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Peptide d
Human CRF
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Human Cyt
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Murine Cy
Human PTP
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Novel non
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Human PTP
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Adc99051 Human KPP
                                     August 17, 2004, 20:45:11; Search time 55 Seconds (without alignments) 2352.850 Million cell updates/sec
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1 MSRSLDSARSFLERLBARGG......NLRIGRPKGPRDPPAEWTRV
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Abr52340 B
Aay28653 B
Aay28654 Aay28654 Aay28654 B
Aaw12522 B
Aay25156 B
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Aab08487 |
Abp07829 |
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                               1586107 seqs, 282547505 residues
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                         using sw model
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AAW37255
AAW49906
AAW71596
AAY81930
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ABP07829
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AAG78623
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AAG78282
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Gapop 60.0 , Gapext 60.0
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11. geneseqp1980s:*

21. geneseqp1980s:*

22. geneseqp2000s:*

43. geneseqp2001s:*

54. geneseqp2001s:*

65. geneseqp2003as:*

77. geneseqp2003as:*
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AAY67255	AAY67254	AAW35301	ADC64297	AAB59383	ABM78984	AAW35300	AAG78268	AAG78281	AAW18093	AAW35302	AAY81783	AAY56098	AAW35298	AAM23746	AAU14379	AAW25172	ABB57374	AAY67250	AAY67252
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10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
				30						36	37	38	ტ	40	41	42	43	44	45

## ALIGNMENTS

Brain derived phosphatase 1; BDP-1; human; receptor; protein tyrosine phosphatase; signal transduction; therapy; diagnosis. Human brain derived phosphatase 1 (BDP-1) AAW49908 standard; protein; 458 AA 96US-0019629P. 96US-0023485P. 96US-0030860P. 96US-0030964P. 96US-0034286P. 97WO-IB000946. (first entry) 17-JUN-1996; 09-AUG-1996; 13-NOV-1996; Homo sapiens WO9748723-A2 17-JUN-1997; 15-NOV-1996; 19-DEC-1996; 20-JUL-1998 24-DEC-1997 AAW49908;

PLANCK GES FOERDERUNG WISSENSCHAFTEN (PLAC ) MAX Nayler O;

Ullrich A, Kharitonenkov AI, Aoki N, Wang HY, Chen Z, Kim YW;

WPI; 1998-120302/11. N-PSDB; AAV17099.

New phosphatase and kinase enzyme(s) - useful in the diagnosis and treatment of signal transduction disorders.

Claim 11; Fig 3a-d; 138pp; English.

This polypeptide comprises a novel human protein tyrosine phosphatase (PTP), designated brain derived phosphatase 1 (BDP-1), that its expressed in most tissues and cell lines at basal level, but expressed high in epithelium origin cell lines and cancer cell lines. The amino acid sequence was deduced from a cDNA clone (see AAV17099) isolated from a hamaropoietic MEGOL CDNA library. The invention relates to novel proteins (see AAW49906-14) involved in cellular signal transduction and to the nucleic acids (see AAV17097-99) coding for them, and provides

Aay81933 Aab08490

AAW71599 AAY81933 AAB08490

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian; nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic; immunosuppressive; antiarthmyroid; cytostatic; hepatotropic; dermatological; antidabetic; nephrotropic; antigout; thyromimetic; neuroprotective; osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoriatic; virucide; opthalmological; antirheumatic; haemostatic; antibacterial; virucide; protozoacide; fungicide; kinase; phosphatase; KPP; call proliferative disorder; atherosclerosis; cirrhosis; hepatitis; cancer; developmental; mental retardation; neurological; halledimertal; antipamente; autoimmune; inflammatory; Crohn's; diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan; helminthic infection; transgenic; gene therapy; human; enzyme.
                                                                                                                                                                                                                                                                                                                             101 YIATQGPLPHTLIDFWRLVWEFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCIT 160
                                                                                                                                                                                                                                                                                                                                                                                                             220
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                                                                                                                                                                                                                                                    KADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLA 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 SVPGSPGHAMADTYAEEQKRGAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAH 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401 AEDARGTLPGRVPADQSPAGSGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
vectors, host cells, purified recombinant proteins, methods for identifying compounds that activate or inhibit the novel proteins, as well as methods for the diagnosis and treatment of diseases associated
                                                                                                                                                                                                               41 KADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLA
                                                                                                                                                                                                                                                                                                                                                                      LIKEKWINEDIMIRTIKVTFOKESRSVYQLOYMSWPDRGVPSSPDHMLAMVEEARRLQGS
                                                                                                                                                                                                                                                                                                                                                                                          YRFLYHTVAQMFCSTLQNASPHYQNIXENCAPLYDDALFLRTPQALLAIPRPPGGVLRSI
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                                                                                                                                                                           Gaps
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                                                                                                                                    91.3%; Score 418; DB 2; Length 458; 100.0%; Pred. No. 0; ive 0; Mismatches 0; Indels
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Best Local Similarity 100.0
Matches 418; Conservative
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                                            well as methods for the with the novel proteins
                                                                                                   Sequence 458 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel isolated polypeptide which is a human kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides, pagnists and antagonists are useful for diagnosing, treating or preventing cell proliferative disorders such as atherosclerosis, cirrhosis, hepatitis and cancer, developmental disorders e.g. mental Parkinson's disease and isorders including Alzheimer's disease and Parkinson's disease and diabetes mellitus and finally, viral, bacterial, fungal, parasitic, protozoan or helmitchic infections. Furthermore, the polynucleotides encoding KPP may be useful for creating transgenic animals to model human disease, as well as during gene therapy procedures. The current sequence is that of the human KPP protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91
                                                                                                                                                                                                           Ή
                                                                                                                                                                                                                                                                                                                       New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Non-receptor protein tyrosine phosphatase, hematopoietic stem cell;
PTP HSC; progenitor cell; tyrosine phosphatase domain; PTP HSC agonist;
                                                                                                                                                                    Arvizu CS;
Tang YT;
Yao MG, Yue H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 SLFDVVLKMRKQRPAAVQTEBQYRFLYHTVAQMFCSTLQNASPHYQNIKENCAPLYDDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 KRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 KRCERYWAQEQEPLQTGLFCITLIKEKWINEDIMLRTLKVTFQKESRSVYQLQYMSWPDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 GVPSSPDHMLANVEBARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLLTQMIPPDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 GVPSSPDHMLAMVEBARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDF
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                                                                                                             Duggan BM;
E, Griffin JA;
ee EA, Lee SY;
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47.4%; Score 217; DB 7; Length 353;
Best Local Similarity 100.0%; Pred. No. 1.5e-203;
Matches 217; Conservative 0; Mismatches 0; Indels
                                                                                                           Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan Emerling BM, Forsythe IJ, Gandhi AR, Gorvad AB, Grif Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lindquist EA, Lu DAM, Marquis UP, Nguyen DB, Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Partial human non-receptor tyrosine phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 4; 424pp; English.
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13-NOV-2001; 2001US-0333098P.
16-NOV-2001; 2001US-0332424P.
30-NOV-2001; 2001US-0334288P.
                                                                           (INCY-) INCYTE GENOMICS INC.
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N-PSDB; ADC99103.
                                                                                                                                                                                                                                                                                                                                                                                        cancer or hepatitis.
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C; also

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/note= "homologous to a nuclear localization signal found on murine PTP PEP"
                   ---- receptor process tyrosine phosphatase; hematopoietic stem cell; PTP HSC; progenitor cell; tyrosine phosphatase domain; PTP HSC agonist; tyrosine dephosphorylation; tyrosine phosphatase; PTP HSC antagonist; stem cell differentiation.
Novel non-receptor tyrosine phosphatase of hematopoietic stem cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haematopoietic stem cell non-receptor protein tyrosine phosphatase -
useful for expansion of undifferentiated stem cells in cell culture.
                                                                                                                                                                                        /note= "phosphorylated by protein kinases A and appears to negatively regulate PTPase activity" 229
                                                                                                                                                                                                                                                      312. .428
/note= "Pro, Ser and Thr rich region"
                                                                                                                                                                                                                                         note= "active site cysteine residue"
                                                                                                                                                   . .303
note= "tyrosine phosphatase domain"
                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Fig 1; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        97WO-US005278.
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N-PSDB; AAV03112.
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                                                                                                                                                                                                                                                                                                                                               WO9735019-A1
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Matches
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   à
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                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a partial human non-receptor protein
tyrosine phosphatase of hematopoietic stem cells (PTP HGC). This protein
tyrosine phosphatase din early hematopoietic stem cells (HSGS) or
progenitor cells, and lacks expression in adult tissues. The protein has
a N-terminal tyrosine phosphatase domain, followed by a region rich in
serine, threonine and proline and a C-terminal region of about 15.25
amino acids which is rich in basic amino acid residues. The protein is
capable of tyrosine dephosphorylation in hematopoietic progenitor cells,
and functional derivatives of such matic tyrosine phosphatase. The
phosphatase domain of the PTP HGC or a PTP HGC-expressing HGC or
progenitor cell can be used in an assay for the identification of PTP HGC
antagonists or agonists. The antagonist can be used to induce the
differentiation of stem cells, such as undifferentiated malignant
hematopoietic cells, e.g. leukaemia cells, which may facilitate their
treatment. The PTP HGC or an agonist antibody against the PTP HGC can be
can agonist on fundifferentiated stem cells in cell culture
(this allows expansion of undifferentiated stem cells in cell culture
hematopoietic growth factor can be used for the expansion of
hematopoietic growth factor can be used for the expansion of
hematopoietic growth factor can be used for the expansion of
hematopoietic growth factor can be used for the expansion of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 ARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILS
tyrosine dephosphorylation, tyrosine phosphatase, PTP HSC antagonist, stem cell differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                  Haematopoietic stem cell non-receptor protein tyrosine phosphatase - useful for expansion of undifferentiated stem cells in cell culture.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.8%; Score 155; DB 2; Le
100.0%; Pred. No. 3.9e-143;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW37254 standard; protein; 453 AA.
                                                                                                                                                                                                                                                                                                                                               Claim 9; Fig 8; 66pp; English.
                                                                                                                                  97WO-US005278.
                                                                                                                                                              96US-00620526.
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                                                                                                                                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                      WPI; 1997-480224/44.
                                                                                                                                                                                                                      Lasky LA, Cheng J;
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es 155; Conserv
                                                                                                                                                                                                                                                                     N-PSDB; AAV03128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 155 AA;
                                            Homo sapiens
                                                                                                                                                              22-MAR-1996;
                                                                       WO9735019-A1
                                                                                                                                17-MAR-1997;
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                                                                                                     25-SEP-1997,
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ID AAW
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AC AAW
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The present sequence represents a novel murine non-receptor protein
tyrosine phosphatase of hematopoietic stem cells (PTP HSC). This protein
is predominantly expressed in early hematopoietic stem cells (HSCs) or
progenitor cells, and lacks expression in adult tissues. The protein has
a N-terminal tyrosine phosphatase domain, followed by a region rich in
serine, threonine and prolline and a C-terminal region of about 15-25
amino acids which is rich in basic amino acid residues. The protein is
capable of tyrosine dephosphorylation in hematopoietic progenitor cells,
and functional derivatives of such native tyrosine phosphatases. The
phosphatase domain of the PTP HSC or a PTP HSC-expressing HSC or
progenitor cell can be used in an assay for the identification of PTP HSC
antagonists or agonists. The antagonist can be used to induce the
differentiation of stem cells, such as undifferentiated malignant
hematopoietic cells, e.g. leukaemia cells, which may facilitate their
the PTP HSC or an agonist em cells in cell culture
the allows expansion of undifferentiated stem cells in cell culture
(this allows expansion of HSC prior to autologous or heterologous bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              marrow transplantation), while the agonist antibody along with a hematopoietic growth factor can be used for the expansion of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     undifferentiated stem cells in vivo
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Mouse; tyrosine phosphorylated cleavage furrow-associated protein; PSTPIP; PBST family; protein tyrosine phosphacase; murine; polymerisation; actin monomer; eukaryotic cell; identification; antagonist.
                                                                 Protein tyrosine phosphatase peptide PTP HSCF.
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                                                                                                                                                                                                                                                                                                                98WO-US001774
                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20 AA;
                                                                                                                                                                                                                                                                                                              30-JAN-1998;
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29-SEP-1997;
                               24-NOV-1998
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                                                                                                                                                                                                                                                                              13-AUG-1998
                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Lasky LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY81930;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This polypeptide comprises a novel rat protein tyrosine phosphatase, designated PTP20, that regulates growth factor stimulation of cellular differentiation. Its amino acid sequence was deduced from a cDNA clone (see AAV17097) isolated from a rat phaecohromocytoma PCI2 cDNA library by PCR amplification using primers based on consensus sequences (see AAW190915-16) of known PTPs. The invention relates to novel proteins (see AAW19096-14) involved in Cellular signal transduction and to the nucleic acids (see AAV17097-99) coding for them, and provides vectors, host calls, purified recombinant proteins, methods for identifying compounds cativate or inhibit the novel proteins, well as methods for the diagnosis and treatment of diseases associated with the novel proteins. For PTP20, activators may act as anti-cancer therapeutic final section of useful for treatment injuries by delaying the differentiation of transplanted neuronal stem cells until they are firmly grafted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nayler 0;
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                                                                                                                                                                                                           Protein tyrosine phosphatase; PTP20; rat; signal transduction; cell differentiation; cancer; neural injury; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.3%; Score 29; DB 2; Length 453; 100.0%; Pred. No. 2.7e-19; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen Z,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment of signal transduction disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     430 GAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAQTGGLGFNLRIGRPKGPRDPPAEWTRV 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kharitonenkov AI, Aoki N,
                                                                                                                                                                           Rat protein tyrosine phosphatase PRP20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New phosphatase and kinase enzyme(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Fig la-b; 138pp; English.
                                                                     AAW49906 standard; protein; 453 AA.
                                                                                                                                                                                                                                                                                                                                                                                                      96US-0019629P.
96US-0023485P.
96US-0030860P.
96US-0030964P.
                                                                                                                                                                                                                                                                                                                                                                        97WO-IB000946.
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N-PSDB; AAV17097.
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Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 453 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-1996;
13-NOV-1996;
15-NOV-1996;
                                                                                                                                                                                                                                                                                                   W09748723-A2
                                                                                                                                                                                                                                                                                                                                                                        17-JUN-1997;
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                                                                                                                                          20-JUL-1998
                                                                                                                                                                                                                                                                                                                                    24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ullrich A,
Kim YW;
                                                                                                                                                                                                                                                                 Rattus sp.
                                                                                                        AAW49906;
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The present sequence represents a peptide from the present invention which describes murine tyrosine phosphorylated cleavage furrow-sacotated protein (BSTPIP), which is a PSST-type protein tyrosine phosphatase (PTP)-interacting polypeptide. PSTPIP induces the polymerisation of actin monomers in a eukaryotic cell, by introducing a vector containing the nucleic acid sequence encoding PSTPIP into the cell. Assays for identifying (ant) agonists of PSTPIP comprise contacting PSTPIP with the agent and monitoring the ability of PSTPIP contacting actin polymerisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                            New PEST-type protein tyrosine phosphatase interacting polypeptide nucleic acids and vectors, for inducing the polymerisation of actin monomers in eukaryotic cells and identifying antagonists.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.4%; Score 20; DB 2; Length 20; 100.0%; Pred. No. 1.1e-11; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                      Disclosure; Page 37; 111pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide fragment of PXXP-HSCF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                            Dowbenko DJ;
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                    WPI; 1998-447234/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
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AAW71596 standard; peptide; 20 AA.

AAW71596 ID AAW7 RESULT

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1 GFNLRIGRPKGPRDPPAEWT
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29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.09
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shimkets RA, Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myasthenia gravis
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                                                                                                                                                                                                                                                                                                                                            Sequence 20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                          This sequence represents a fragment of a protein tyrosine phosphatase (PTP). It was used to isolate the PST phosphatase interacting protein (PSTPIP) sequence of the invention. The protein is a protin tyrosine phosphatase that possesses a non-catalytic domain comprising a proline, serine and threonine rich region and a C-terminal segment of 20 amino acid (as's) rich in proline, and defines an SH3 binding domain. Nucleic acids encoding native PSTPIP molecules can be used to isolate homologous specifically expressed in tumour cells, which might provide more specific targets for tumour therapy. The DNA is also useful for the preparation of PSTPIP polypeptides by recombinant techniques and as hybridisation probes for searching cDNA and genomic libraries for the coding sequence of other PSTPIP polypeptide analogues in other species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein tyrosine phosphatase; PTP; phosphatase interacting protein; PSTPIP; PEST family; protein tyrosine phosphatase; actin monomer; tissue typing; tumour cell; tumour imaging.
                                                                                                                                                            Novel genes encoding protein tyrosine phosphatase binding proteins for isolating homologous genes, e.g. in tumor cells, which provide specific targets for tumor therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.4%; Score 20; DB 3; Length 20; 100.0%; Pred. No. 1.1e-11; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide derived from a protein tyrosine phosphatase.
                                                                                                                                                                                                                 Disclosure; Col 35; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        437 GENLRIGRPKGPRDPPAEWT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB08487 standard; peptide; 20 AA
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                          97US-00938830
                                                    97US-0104590P.
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Best Local Similarity 100.0
Matches 20, Conservative
                                                                                                        Dowbenko DJ, Lasky LA;
                                                                              (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 AA;
                          29-SEP-1997;
                                                    17-APR-1997;
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21-MAR-2000
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propopheres interacting process.

Mandesd-90 acperates interacting process.

Ablossary of care interacting process.

CC (FTP). They were used to identify interaction domains of a murina protein (1972PP).

Provisine phosphatese (FTP) biopphases (FTP) propphases (FTP) propphases
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Treferred to as open reading frame. ORFX, where X is 1-11491 (see Table In the specification). ABN15762 to ABN2752 encode the human ORFX proteins are useful for proteins given in ABN15762 to ABN2752 encode the human ORFX reating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manifacture of a medicament for treating a syndrome associated with ORFX sequences can be used in Gene therapy. ORFX sequences can be used in Gene therapy. ORFX sequences can be used in Gene therapy. ORFX sequences can be used in the special carrier of standards in the sequences can be used in the sequences can be used in the treatment of cancer, hyperproliferative disorders related to organ transplantation, cardiovascular diseases, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol eter storage disease, various immune disorders substanting and isorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune inflammatory eve disease. ORFX proteins are also useful for treating disorders, including from the purns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form part directly from WIPO at fibrosic, introduces and electronic sequences are also sequences and electronic sequences and electronic sequences are dispersed to the printed specification, but was obtained 
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                                                                                                                                                            present invention describes substantially purified human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
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                                                                                                           Disclosure, SEQ ID NO 15640; 1037pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP04248 standard; protein; 60 AA.
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29-AUG-2000; 2000US-0228716P.
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Best Local Similarity 100.'
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 VHCSAGCGRTGV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VHCSAGCGRTGV 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 64 AA;
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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27252 encode the human ORFX in the specification). ABN15762 to ABN27252 encode the human ORFX corporation of treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polymucleotide squences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, infribosis of liver, protective in the contains, benign tumours, keloid, degenerative disorders, hemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiorascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious disease, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease, autoimmune disorders such as multiple sclerosis, theumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune disorders such as multiple sclerosis, contains are also bene degenerating during, incisions, there in the prince of protection or regeneration and treatment of lung or liver fibrosis, protection or regeneration and treatment of lung or liver fibrosis, contains protein contains and conditions resulting from reperferion or regeneration stissues and conditions resulting from cyclokine damage. Na. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic contains and decomposity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                              Novel human polypeptides and polynuclectides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.4%; Score 11; DB 5; Length 60; 100.0%; Pred. No. 0.019; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                      Disclosure, SEQ ID NO 8478; 1037pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB59384 standard; protein; 242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0137319P.
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                 Shimkets RA, Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KARYKDVLPYD
                                                           WPI; 2002-106308/14.
N-PSDB; ABN20000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 60 AA;
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16-JUN-1999;
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(COLD-) COLD SPRING HARBOR LAB.

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ABR52340;
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ABRES 23440
ID ABRES 23440
NX XX XX ABRES 19-40
NX ID-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to identifying agents which alter the interaction between a protein tyrosine phosphatase (PTP) and a tyrosine phosphatase (PTP) and a tyrosine phosphatylated using fluorescence energy signals. The methods are useful for performing screening assay to identify agents that alter Prb binding to and PTP-mediated catalytic dephosphorylation of phosphotyrosine peptide substrates. The present sequence is that of catalytic domain of a PTP for comparison with human PTPIB (AAG78262)
                                                                                                                                                                                                                                     The present invention provides substrate trapping mutant protein tyrosine phosphatases (PTPs). They can be used to reduce the activity of tyrosine phosphorylated proteins and to screen for modulators capable of altering the binding of protein tyrosine phosphatases to their substrate. These may be used in disease diagnosis and treatment
                                                                                                        New substrate trapping mutant protein tyrosine phosphatases (PTP) in which the wild type PTP catalytic domain invariant aspartate is replaced with an unphosphorylated amino acid, useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTP; protein tyrosine phosphatase; tyrosine phosphorylated polypeptide; dephosphorylation; phosphotyrosine; human; PTP1B; mouse; fruit fly;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening assays to identify agents that alter protein tyrosine phosphatase (PTP) binding to, and PTP-mediated catalytic dephosphorylation of phosphotyrosine peptide substrates.
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100.0%; Pred. No. 0.065;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG78282 standard; protein; 291 AA
                                                                                                                                                                                           Disclosure, Fig 1; 109pp; English
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Best Local Similarity lov...
Local Similarity lov...
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                                                                WPI; 2001-080598/09
                    Zhang S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CEPT-) CEPTYR INC.
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 242 AA;
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                    Tonks NK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG78282;
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Sequence 291 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antiproliferative, hepatotropic; nephrotropic; antiarthritic; antiprofiatic; cardiant; cytostatic; gene therapy, liver disease; proliferative disorder; renal failure; cardiovascular disorder; immunological disorder; antibritis; psoriasis; congenital heart defect; congestive heart failure; cancer; human; mouse; yeast; rat; fruitfly.
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                                                         Gaps
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Bassolino
                                                         ·;
Length 291;
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Todderud CG,
2.4%; Score 11; DB 4; Length 291
100.0%; Pred. No. 0.077;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein relating to the invention SEQ ID NO: 29.
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Finger J, Tc,
, Banas D;
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100.0%; Pred. No.
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Bol D, Schieven G, F
Mcatee P, Suchard S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001US-0280186P.
01-MAY-2001; 2001US-0287735P.
05-UTN-2001; 2001US-028648P.
25-UTN-2001; 2001US-0300465P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                            11; Conservative
                                                                                                                     69
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                                                                                                                  59 KNRYKDVLPYD
                                                                                                                                                                        KNRYKDVLPYD
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Query Match
Best Local Similarity
Matches 11; Conserv
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Best Local Similarity
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Siemers N, E
Krystek S, N
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to treat autoimmune diseases and transplant situations
                         Sequence 692 AA;
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                                                                                                                                                                                                                                                                                                                                                                                               29-OCT-1999;
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                                                                                                                                                                                                                  AAG78623;
                                                Query Match
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                                                                                                                                                                  RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding intracellular tyrosine phosphatase and related proteins, used to modulate signaling through T cells, particularly as immunosuppressant.
                                                                                                                                                                                                                 Lymphoid Protein Tyrosine Phosphatase; Lyp protein; immunosuppressant; intracellular tyrosine phosphatase; PrPase; fetal liver; transplant; resting lymphoid cell; protein tyrosine kinase; PTKs; lymphocyte; T cell antigen receptor signalling; cytokine receptor signalling; autoimmune disease; intronic sequence; alternative mRNA splicing.
                                                                                                                                                                                                                                                                                                                                                                                  469. .472

/label= NXXY_motif

/note= "Unique sequence recognised by phosphotyrosine

binding (PTB) domain"

615. .623

/label= SH3 binding site

/note= "Proline rich sequence"
                                                                                                                                                                                                                                                                                                                                         //label= PrPase domain
/note= "Single_catalytic protein tyrosine phosphatase
    Gaps
  ö
    Indels
  ;
                                                                                                                                                                                           Human Cytoplasmic phosphatase, Lyp2 protein.
    Mismatches
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                 AAY28653 standard; protein; 692 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4b; Page 55; 105pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-CA000038
                                                                                                                                                                  (first entry)
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    Conservative
                           227 VHCSAGCGRTG 237
                                            225 VHCSAGCGRIG 235
                                                                                                                                                                                                                                                                                                                                                                      domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-444404/37.
N-PSDB; AAX90696.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Binding-site
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                                                                                                                                                                  01-OCT-1999
  11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roifman CM
                                                                                                                                         AAY28653;
                                                                                                                                                                                                                                                                                                                        Key
Domain
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                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides the protein and coding sequences of human tyrosine phosphatase hPTP. The protein is expressed in human normal suprarenal tissue. The present sequence is the protein of the invention
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein tyrosine phosphatase and its coding sequence
  Length 692;
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                                     Indels
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100.0%; Pred. No. 0.19;
iive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 12-13 (Disclosure); 29pp; Chinese.
  DB 2;
0.17;
2.4%; Score 11; DB 100.0%; Pred. No. 0.1; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: August 17, 2004, 20:51:35 Job time : 57 secs
                                                                                                                                                                                                                  AAG78623 standard; protein; 799 AA.
                                                                                                                                                                                                                                                                                                                                                                          Human; tyrosine phosphatase; hPTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99CN-00119935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99CN-00119935.
                                                                                                                                                                                                                                                                                                                                       Human tyrosine phosphatase.
                                                                                                                                                                                                                                                                                               (first entry)
                  Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 11, Conservative
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                                                                               228 HCSAGCGRIGV 238
                                                                                                                  236
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                                                                                                                  226 HCSAGCGRTGV
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Sequence 4, Appli Sequence 7, Appli Sequence 7, Appli Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 22, Appli Sequence 1, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 3, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli			ength 155; Indels 0; Gaps 0;	WRKORYKDVLPYDQTRVILS 76	LPHTLLDFWRLVWEFGVKVILMACREIEN 136 		
US-08-811-481-4 US-09-876-527-4 US-09-876-527-4 US-09-876-527-7 US-09-876-527-2 US-08-811-481-2 US-08-811-22 US-08-811-22 US-08-811-22 US-08-811-22 US-08-811-22 US-08-811-3-1 US-08-548-159-1 US-08-548-159-1 US-08-548-159-1 US-08-548-159-1 US-08-548-159-1 US-08-548-159-1 US-08-548-159-1 US-08-11-481-16 US-08-876-527-16 US-08-41-464-3 US-08-416-669-3 US-08-348-0068-5 US-08-348-0068-5	ALIGNMENTS	US/08821278A nnce A. tein Tyrosine Phosphatases ser. US/08/821,278A 197-03-20	; Score 155; DB 3; I %; Pred. No. 1.9e-134; 0; Mismatches 0;	ARGGREGAVLAGEFSDIQACSAAMKADGVCSTVAGSRPENVRKNRYKOVLPYDQTRVIL: 	LLQEBGHSDYINGNPIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVI 	GRKRCERYWAOEOEPLOTGLFCITLIKEKWLNEDI 171 	821278A
2299 3298 3246 3246 3246 3246 326 326 326 326 326 326 326 326 326 32		ication US/00 DN: DN: 3, Jill 4, Laurence 2 V. Laurence 2 DN: Protein P100N NUMBER: 1 NUMBER: 1997-00 NOS: 23	33.8% 100.0 vative	LAGEFSDI(         LAGEFSDI(	YINGNFIR          YINGNFIR	GRKRCERYWAQEQEPLQTGLF 	278A-2 2. Application US/08821278A 10. 6288902 INFORMATION: NIT: Cheng, Jill
		1-278A-17 No. 6238902 No. 6238902 No. 6238902 No. 6238902 No. 623802 No. 1 Lasky, Laurenco OF INVERTION: Protect REFERENCE: P1010R1 WT PELING DATE: 1997 WT PILING DATE: 1997 RY FILING DATE: 1997 RY FILING SAPER PRINGE: 1997 RY FILING SAPER RY FILING SAPE	ı, milarity Conser	RGGREGAV           RGGREGAV	LQEEGHSD          LQEEGHSD	RKRCERYW          BRKRCERYW	.2 Applicati 238902 WMATION: Cheng, J
000000000000000000000000000000000000000		TOZ KKOMPE ZE H	atch al	4 71 	77 [	137 G	SULT 2 -08-821-278A-2 Sequence 2, Ap Patent No. 623 GENERAL INFORM
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		RESULT 1 US-08-821 Sequence   Parent	Query Best Match	& g	ර් යි	o o	RESULT 2 US-08-821- ; Sequence ; Patent ; GENERAL
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Sequence 7, Application US/09430626A Patent No. 6482605 GENERAL INFORMATION;
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0
                                                                                                                                                                                                                                           Sequence 7, Application US/08951260A
| Patent No. 6004791
| GENERAL INFORMATION:
| APPLICANT: AOKi, Nachito |
| APPLICANT: AOKi, Nachito |
| TILLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20 |
| TITLE OF INVENTION: AND RELATED PRODUCTS AND METHODS |
| NUMBER OF SEQUENCES: 7 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Loyon & Lyon |
| STREET: 633 West Fifth Street |
| STREET: Los Angeles |
| STREET: California |
| STATE: California
                                                     Query Match
7.0%; Score 32; DB 3; Length 453;
Best Local Similarity 100.0%; Pred. No. 4.1e-21;
Matches 32; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.3%; Score 29; DB 3; Length 453
Best Local Similarity 100.0%; Pred. No. 2.3e-18;
Matches 29; Conservative 0; Mismatches 0; Indels
                                                                                                                                                       100 AYIATQGPLPHTLLDFWRLVWEFGVKVILMAC 131
                                                                                                                             100 AYIATQGPLPHTLLDFWRLVWEFGVKVILMAC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAQTGGLGFNLRIGRPKGPRDPPAEWTRV 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 227/004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELERX: 67-3510
INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       453 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: peptide US-08-951-260A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
     ; ORGANISM: Mus Musculus
US-08-821-278A-2
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                RESULT 3
US-08-951-260A-7
                                                                                                                                                        g
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RESULT 4 US-09-430-626A-7

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TITLE OF INVENTION:

MUDIECANT: Acki, Mechitch

MUDIECANTER: Acki, Mechitch

MUDIECANTON MARTHER: Acki, Mechitch

MUDIECANTON MARTHER: Acki, Mechitch

MARTHER MARTHER: Ac
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us-10-087-993a-36.olig.rai
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Gaps · 0

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2.4%; Score 11; DB 2; Length 231; 100.0%; Pred. No. 0.042; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                           Query Match
4.4%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KESULT /
US-08-446-345-37

Sequence 37, Application US/08446345

Patent No. 5831009

PAPLICANT: Woller, Mael

APPLICANT: Moller, Mael B. H.

APPLICANT: Moller, Mails P.H.

APPLICANT: Moller, Marin B.

TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE

TITLE OF INVENTION: PHOSPHATASES PTP-D1

NUMBER OF SEQUENCES: 41

CORDESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

STREET: N.Y.

COUNTRY: U.S.A.

COUNTRY: U.S.A.

COUNTRY: IBM PC compatible

COMPUTER: IBM PC and A135

SOFTWARE: Patentin PRelease #1.0, Version #1.25

CLASSIFICATION NUMBER: US/08/446,345

FILING DATE: 22-MAY-1995

CLASSIFICATION NUMBER: US 08/234,440

FILING DATE: 28-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: COPILIZI, LAURA A.35

REFERENCE/DOCKET NUMBER: 30'42

REFERENCE/DOCKET NUMBER: 30'42

REFERENCE/DOCKET NUMBER: 30'42

TELECOMMUNICATION NUMBER: 30'42

TELECOMMUNICATION NUMBER: 30'42

REFERENCE/DOCKET NUMBER: 30'42

TELECOMMUNICATION NUMBER: 30'42
                                                                                                                                                                                                                                                                                                                          437 GENLRIGRPKGPRDPPAEWT 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERICTICS:
LENGTH: 231 amino acids
                            20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 231 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TYPE: LINKNOWN
; INFORMATION FOR SEQ ID NO: 2; SEQUENCE CHARACTERISTICS; LENGTH: 20 amino acids; TYPE: Amino Acid 10S-09-020-222-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.4
Best Local Similarity 100.
Matches 11; Conservative
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MOLECULE TYPE: protein
US-08-446-345-37
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TORRESPONDERS.

CORRESPONDER ADDRESS:
CORRESPONDER ADDRESS:
TORRESPONDER ADDRESS:
TORRESPONDER Francisco
STREET: 1 DNA Way
CITY: South San Francisco
STREET: 1 DNA Way
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.49 Mb floppy disk
COMPUTER: TEM PC compatible
CONFUTER: TEM PC COMPATION
MEDIUCATION NUMBER: US/09/020,222
FILING DATE: 06-Feb-1998
FILING DATE: 06-Feb-1998
TILING DATE: 07/1997

ATTORNEY/AGENT INFORMATION:
NAMBE: DESGEY, GIAGGER R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 20;
                                                                                                       COMPUTER READBLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,830
FILING DATE:
CLASSIFICATION S30
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/798419
FILING DATE:
ATTORNEY/AGBNT INPORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REGISTRATION SOFT-9881
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH 20 amino acids
TELENGTH 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 20; DB 3; L. Pred. No. 2.5e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 4.4%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 2.5 Matches 20; Conservative 0; Mismatches
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REGISTRATION NUMBER: 33,055
REFERENCE-DOCKET NUMBER: P1066r1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
US-09-020-222-20
Sequence 20, Application US/09020222
; Patent No. 6111073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GENLRIGREKGERDEPAEWT 20
        South San Francisco
California
Y: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Amino Acid
                                                                                        94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
        CITY: SOL
STATE: Ca
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-938-830-20
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Matches
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Thu Aug 19 09:28:44 2004

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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA: WS/09/144,925
FILING DATE: US/09/144,925
FILING DATE: US/09/144,92
FILING DATE: US/09/144,92
FILING DATE: US/09/144,92
FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: peptide US-09-144-925-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 KNRYKDVLPYD 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 KNRYKDVLPYD 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-09-848-294-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX:
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0
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                               US-08-685-992-21
Sequence 21, Application US/08685992
Sequence 21, Application US/08685992
Sequence 21, Application US/08685992
SETERAL INFORMATION:
APPLICANT: FIGHT, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
SIRBET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIALIE
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,992
FILING DATE: 25-UUL-1996
CLASSIFCATION: 435
FRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
RAGISTRATION NUMBER: 32.27
REFRENCY/DOCKET NUMBER: CSHL96-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEPHAX: 781-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
           RESULT 8
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.. 0

Gaps

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Sequence 7, Application US/09848294

Sequence 7, Application US/09848294

Patent No. 6479640

GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas K.

TITLE OF INVENTION: Isolation of A cDNA Encoding A No. 6479640el

TITLE OF INVENTION: Protein Tyrosine Phosphotase Which Localizes to Forein Tyrosine Phosphotase Which Localizes to Forein Tyrosine Phosphotase Which Localizes to CURRENT OF INVENTION: Adhesions and Uses Therefor

TITLE OF INVENTION: Adhesions and Uses Therefor

TITLE OF INVENTION: Adhesions and Uses Therefor

FILE REFERENCE: CSH190-04FZA

CURRENT APPLICATION NUMBER: US/09/28,251

PRIOR FILING DATE: 1999-01-22

PRIOR PELING DATE: 1996-12-04

PRIOR APPLICATION NUMBER: 08/107,420

PRIOR APPLICATION NUMBER: 08/107,420

PRIOR APPLICATION NUMBER: 07/663,579

PRIOR APPLICATION NUMBER: 07/663,579

PRIOR APPLICATION NUMBER: 07/643,579

PRIOR APPLICATION NUMBER: 07/494,036

PRIOR FILING DATE: 1991-03-01

PRIOR PRIOR APPLICATION NUMBER: 07/494,036

PRIOR FILING DATE: 1990-03-14

NUMBER OF SEQ ID NOS: 13

SOFTWARE FEASER FEASER FEASER FOR FEASER 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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US-09-848-294-7
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100.0%; Pred. No. 0.13;
ive 0; Mismatches 0; Indels
                                                                                                       2.4%; Score 11; DB 3; Length 802;
100.0%; Pred. No. 0.13;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09081345

Sequence 2, Application US/09081345

Batent No. 622641

GENERAL INFORMATION:

APPLICANT: Bahija Jallal

APPLICANT: Gregory D. Plowman

TITLE OF INVENTION: DIGGNOSIS AND TREATMENT OF

TITLE OF INVENTION: PTP04 RELATED DISORDERS

NUMBER OF SEQUENCES: 18

CORDESSED LYON & LYON

STREET: 613 West Fifth Street

STREET: 613 West Fifth Street

STREET: Galifornia

COUNTRY: U.S.A.

ZIP: 9071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: 815EQ for Windows 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/081,345

FILING DATE: Herewith

CLASSIFICATION NUMBER: 06/047,222

FILING DATE: May 20, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

NAME: Warburg, Richard J.

NAME: Warburg, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 234/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-160
TELEX: (213) 955-0440
TELEX: (273510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 807 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.4
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                        11, Conservative
                                                                                                                                                                                                      228 HCSAGCGRIGV 238
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                     TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-081-345-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
HOLECULE TYPE: peptide
US-09-081-345-2
STRANDEDNESS: single
                                                                                                            Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                   RESULT 13
US-09-081-345-2
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US-09-848-294-2
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                                                                                  US-08-821-278A-18
Sequence 18, Application US/08821278A
Fatent No. 6238902
GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TITLE OF INVENTION: Protein Tyrosine Phosphatases;
FILE REPERENCE: P1010R1
CURRENT APPLICATION NUMBER: US/08/821,278A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 18
LENGTH: 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-081-345-18
; Sequence 18, Application US/09081345
; Patent No. 622841;
; GENERAL INFORMATION:
; APPLICANT: Bahija Jallal
; APPLICANT: Gregory D. Plowman
; TITLE OF INVENTION: PIPO4 RELATED DISORDERS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.4%; Score 11; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 11; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 634 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
CITY: Los Angeles
CONDUTE: California
COUNTR: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: STORME
COMPUTER: FRANCES
COMPUTER: FRANCESC
COMPUTER: FRANCESC
COMPUTER: STORME IBM P.C. DOS 5.0
SOFTWARE: FRANCESC
CURRENT APPLICATION DATA:
FILING DATE: Herewith
CLASSIFCATION NUMBER: US/09/081,345
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047,222
FILING DATE: May 20, 1997
ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 234/253
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELERA: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 HCSAGCGRIGV 238
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KNRYKDVLPYD 14
                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo Sapien
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Sequence 2, Application US/09848294

Fatent No. 6479640

SCREERL INCORMATION:
SCREERL INCORMATION:
SCREERL INCORMATION:
SCREERL INCORMATION:
SCREERL INCORMATION:
TITLE OF INVENTION: Protein Tyrosine Phosphorase Which Localizes to Focal
TITLE OF INVENTION: Adhesions and Uses Therefor
TITLE OF INVENTION: Adhesions and Uses Therefor
FILE REFERENCE: CSHL90-04FZA
CURRENT APPLICATION NUMBER: US/09/848,294
CURRENT FILING DATE: 1999-01-05-03
PRIOR PILING DATE: 1999-01-02
PRIOR PILING DATE: 1999-01-02
PRIOR PILING DATE: 1999-01-03-04
PRIOR PILING DATE: 1999-03-04
PRIOR FILING DATE: 1991-03-01
PRIOR PILING DATE: 1991-03-01
PRIOR PILING DATE: 1991-03-01
PRIOR PILING DATE: 1990-03-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 913
TYPE: PRT
CORGANISM: Homosapiens
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Sequence 23, Application US/08938830

Patent No. 6040437

GENERAL INFORMATION:
APPLICANT: Lasky, Laurence A. APPLICANT: Dowbenke, Donald J. TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage TITLE OF INVENTION: Purrow-Associated Proteins (PSTPIPs)
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS: ADDRESSE: Genentech, Inc. STREET: LD NA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.4%; Score 11; DB 4; Length 913; Best Local Similarity 100.0%; Pred. No. 0.15; Matches 11; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/798419
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISSTRATION NUMBER: 33,055
REFRENCE/DOCKET NUMBER: P1066P1
TELEPHONE: 650/225-3216
TELEPHONE: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   673 KARYKDVLPYD 683
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US-08-938-830-23
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Sequence 12, Appli
Sequence 13, Appli
Sequence 13, Appl
Sequence 22392, A
Sequence 94, Appl
Sequence 819, Appl
Sequence 7, Appli
Sequence 7, Appli
Sequence 93, Appli
Sequence 93, Appli
Sequence 93, Appli
Sequence 22, Appli
Sequence 23, Appli
Sequence 24, Appli
                                                                          August 17, 2004, 20:52:38; Search time 46 Seconds (without alignments) 3125.622 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                             458
1 MSRSLDSARSFLERLEARGG.....NLRIGRPKGPRDPPAEWTRV 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                      Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PET_NEW PUBL.pep:*

3: /cgn2_6/ptodata/1/pubpaa/SET_NEW PUBL.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 US-10-087-993-36
4 US-10-243-687-7
10S-10-340-288-13
4 US-10-340-288-13
10S-09-801-368-280
10S-10-981-368-280
2 US-10-369-493-22392
2 US-10-087-684-94
2 US-10-218-779-94
2 US-10-072-012-819
1 US-09-8468-294-7
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US-10-087-684-93

US-10-218-779-93

US-09-788-626-22

US-10-309-423-4
                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                           1292805 seqs, 313927144 residues
                                                                                                                                                                                                                                                                                                                                                   Post-processing: Listing first 45 summaries
                                                    protein - protein search, using sw model
                                                                                                                                                                                     OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                          length: 0
length: 2000000000
                                                                                                                                 US-10-087-993A-36
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111.
112.
114.
115.
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Maximum DB seq
                                                                                                                                 Title:
Perfect score:
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                                                                                                                                                                                                                                                      Word size :
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                                                                                                                                                                                                                             Searched:
                                                                             Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.
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| 16 | 11 | 2.4 | 703 | 15 | US-10-366-547-40 | Sequence 40, Appl 19 | US-09-822-295-18 | Sequence 55, Appl 19 | US-09-822-295-2 | Sequence 57, Appl 20 | US-09-822-295-2 | Sequence 57, Appl 21 | Z-4 | 802 | IS | US-10-366-547-95 | Sequence 57, Appl 21 | Z-4 | 807 | 9 | US-09-842-295-2 | Sequence 57, Appl 22 | II | Z-4 | 807 | 9 | US-09-848-294-2 | Sequence 27, Appl 22 | II | Z-4 | 913 | 9 | US-09-848-294-2 | Sequence 27, Appl 24 | US-10-369-423-2 | Sequence 27, Appl 24 | US-10-369-423-2 | Sequence 27, Appl 25 | US-09-801-368-282 | Sequence 27, Appl 26 | US-09-801-368-282 | Sequence 27, Appl 27 | US-10-369-433-1750 | Sequence 38, Appl 37 | US-09-801-368-282 | Sequence 38, Appl 37 | US-09-801-368-282 | Sequence 57, Appl 38 | US-09-801-368-282 | Sequence 77, Appl 38 | US-09-801-368-367-37 | Sequence 77, Appl 38 | US-09-801-368-374-38 | Sequence 72, Appl 39 | US-09-801-368-374-38 | Sequence 845, Appl 39 | US-09-
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# ALIGNMENTS

US-10-087-993-36

US-10-087-993-36

US-10-087-993-36

Sequence 36, Application US/10087933

Publication No. US20020169303A1

Application No. USCOORD

RAM, Yeong Woong

Wang, Hong Yang

Charitonenkov, Alexei Igorevich

RADAILON NOVEL PTP20, PCP-2, BDF1, CLK,

AND SIRP POLYPEFIDES AND RELATED

PRODUCTS AND METHODS

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Uyon & Lyon

STREET: 633 West Fifth Street

SUITY: Los Angeles

STREET: California

CONNTRY: US.A.

ZIP: 90071-2066

COMPUTER READABLE PCRM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

SCONMUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: FastSEO for Windows 2.0

CURRENT APPLICATION NUMBER: US/10/087, 993

FILING DATE: 05-MAT-2002

CLASSIFICATION NUMBER: US.08/877,150

FILING DATE: Une 17, 1997

APPLICATION NUMBER: US. 60/019,629

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INFORMATION FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSRSIDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSRSIDSARSFLERLEARGGREGAVIAGEFSDIQACSAWKADGVCSTVAGSRPENVRKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 OXESRSVYQLQYMSWPDRGVPSSPDHMLAMVEBARRLQGSGPEPLCVHCSAGCGRTGVLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTBEQYRFLYHTVAQMFCSTLQNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLPGRVPADQSPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLPGRVPADQSPAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 458;
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TITLE OF INVENTION: AND RELATED PRODUCTS AND METHODS
FILING DATE: June 17, 1996
APPLICATION NUMBER: U.S. 60/023,485
FILING DATE: AUGUST 9, 1996
APPLICATION NUMBER: U.S. 60/030,860
FILING DATE: NO. US20020169303A1ember 13, 1996
APPLICATION NUMBER: U.S. 60/034,286
FILING DATE: December 19, 1996
APPLICATION NUMBER: U.S. 60/030,964
FILING DATE: NO. US20020169303A1ember 15, 1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 458; DB 13; Best Local Similarity 100.0%; Pred. No. 0; Matches 458; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                               NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 225/298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 458 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLGOY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                           TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 36:
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Publication No. US20030073120A1
GENERAL INFORMATION:
APPLICANT: Acki, Nachito
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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Sequence 32, Application US/2000169303A1
GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
Rim, Yeong Woong
Wong, Fong Yang
Chen, Zhengjun
Naylor, Oliver
Kharitonenkov, Alexei Igorevich
Kharitonenkov, Alexei Igorevich
Staritonenkov, Alexei Igorevich
Staritonenkov, Alexei Igorevich
Kharitonenkov, Alexei Igorevich
Spilor, Oliver
PRODUCTS AND METHODS
PRODUCTS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.3%; Score 29; DB 14; Length 453; Best Local Similarity 100.0%; Pred. No. 4.6e-19; Matches 29; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                         CURRENT SYSTEM: IEM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/243,687
FILING DATE: 16-Sep-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/09/430,626A
FILING DATE: 29-Oct-1999
APPLICATION NUMBER: 08/951,260
FILING DATE: October 16, 1997
APPLICATION NUMBER: 60/30,860
FILING DATE: No. US20030073120A1ember 13, 1996
APPLICATION NUMBER: PCT/1897/00946
FILING DATE: June 17, 1997
                                                                                                                      CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         430 GAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
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REFERENCE/DOCKET NUMBER: 227/004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: 2
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
TELEX: 67-3510
WATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 453 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
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                                                                                                     Suite 4700
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APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT FILING DATE: 1001-03-07
PRIOR FILING DATE: 2000-01-03-07
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: 1999-10-20
LENGTHA: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22392, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION
APPLICANT: Co. Yongwei
APPLICANT: Slater, Steven C.
APPLICANT: Goldman Barry S.
APPLICANT: Coldman Barry S.
APPLICANT: Coldman Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
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                                                                                                                                                           4.4%; Score 20; DB 14; Length 20; 100.0%; Pred. No. 1.4e-11; cive 0; Mismatches 0; Indels
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Pred. No. 0.021;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No. US20020128250Alman, Thea
Royer, John
Salama, Sofie
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 280, Application US/09801368
Patent No. US/20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Busby, Robert
APPLICANT: Hecht, Peter
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Mine, Todd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; ORGANISM: Saccharomyces cerevisiae US-09-801-368-280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.6%; Scc...
100.0%; Pre
                                                                                                                                                                                                                                                       263 VVLKMRKORPAAVOTEEOYR 282
                                                                                                                                                                                                                                                                                                   1 VVLKMRKORPAAVOTEEOYR 20
SOFTWARE: Patentin version 3.2 SEQ ID NO 13 LENGTH: 20
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                                                                                                                                                                                   Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sherman, Amir
Silva, Jeff
                                                                    TYPE: PRT
CORGANISM: Homo sapiens
US-10-340-288-13
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Best Local Similarity
Matches 12; Conserv
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US-10-369-493-22392
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APPLICANT:
APPLICANT:
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APPLICANT:
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RESULT 4
RESULT 4
SEQUENCE 13, Application US/10340288
SEQUENCE 13, Application No. US20030170855A1
SEQUENCE 13, Application No. US20030170855A1
SEQUENCE 13, Application No. US20030170855A1
SEPLICANT: Albert Einstein College of Medicine of Yeshiva University
APPLICANT: ZHANG, ZEONG-Yin
APPLICANT: ZHANG, ZEONG-Yin
APPLICANT: ZHANG, ZEONG-YIN
TILLE OF INVENTION: MUTANT AND USES THEREOF
TILLE OF INVENTION: MUTANT AND USES THEREOF
FILE REPERBENCE: 967007/792
CURRENT APPLICATION NUMBER: US/10/340,288
CURRENT FILING DATE: 2003-01-10
PRIOR FILING DATE: 2003-01-17
NUMBER OF SEQ ID NOS: 37
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PRIOR APPLICATION NUMBER: US/08/877,150

FILING DATE: June 17, 1997

APPLICATION NUMBER: US. 60/019,629

FILING DATE: June 17, 1996

APPLICATION NUMBER: US. 60/023,485

FILING DATE: No. US2002169303A1ember 13, 1996

APPLICATION NUMBER: US. 60/034,286

FILING DATE: December 19, 1996

APPLICATION NUMBER: US. 60/034,286

FILING DATE: December 19, 1996

APPLICATION NUMBER: US. 60/030,964

APPLICATION NUMBER: US. 60/030,964

APPLICATION NUMBER: US. 20/030,964

ATTORNEY/AGENT INFORMATION:
NAME: WAZDHING, NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 225/298

TELEBERAI: (213) 489-1600

TELEBERA: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.2%; Score 24; DB 13; I Best Local Similarity 100.0%; Pred. No. 3.2e-14; Matches 24; Conservative 0; Mismatches 0;
                                                                 STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/087,993
FILING DATE: 05-Mar-2002
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
  STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 AYIATQGPLPHTLLDFWRLVWEFG 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 453 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                           storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 32: SEQUENCE CHARACTERISTICS:
                          Suite 4700
                                           CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 67-3510
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Gaps

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## APPLICANT: Guo, Xiacjia
## APPLICANT: Miller, Charles
## APPLICANT: Miller, Charles
## APPLICANT: Miller, Charles
## APPLICANT: Miller, Esha
## TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
## TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
## TITLE OF INVENTION: 2140-214
## CURRENT FILING DATE: 2002-10-39
## PRIOR PILING DATE: 2000-11-30
## PRIOR APPLICATION NUMBER: 60/250,-926
## PRIOR APPLICATION NUMBER: 60/264,180
## PRIOR APPLICATION NUMBER: 60/364,180
## PRIOR PELING DATE: 2001-01-25
## PRIOR PELING DATE: 2001-01-25
## PRIOR PELING DATE: 2001-01-05
## PRIOR PELING DATE: 2001-06-20
## NUMBER OF SEQ ID NOS: 216
## SEQ ID NO 94
## LENGHAL 235
## TITLE OF THE PERIOR DATE: 2001-06-20
## SEQ ID NO 94
## LENGHAL 235
## TITLE OF THE PERIOR DATE: 2001-06-20
## SEQ ID NOS: 216
## SEQ ID N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.4%; Score 11; DB 12; Length 235; Best Local Similarity 100.0%; Pred. No. 0.07; Matches 11; Conservative 0; Mismatches 0; Indels
                      2.4%; Score 11; DB 12; Length 235; 100.0%; Pred. No. 0.07; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 94, Application US/10218779 Publication No. US20040029222A1 GENERAL INFORMATION:
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Padigaru, Muralidhara
Mishra, Vishuu
Patturajan, Meera
Shenoy, Suresh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ellerman, Karen
Stone, David
Gerlach, Valerie
Grosse, William
Alsobrook II, John
Lepley, Denise
Rieger, Daniel
Burgess, Catherine
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Tchernev, Velizar
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APPLICANT: MacDougall, John
APPLICANT: Millet, Isabelle
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Spytek, Kimberly
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Malyankar, Uriel
Guo, Xiaojia
               Query Match
Best Local Similarity 100.0
Matches 11; Conservative
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Boldog, Ferenc
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CORGANISM: Homo sapiens
US-10-218-779-94
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APPLICANT:
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-gred, Suresh G.

-greelli, Luca

-greelli, Luca

-greelli, Luca

-green, Velizar T.

-green, Vernet, Corine A.M.

-green, Majola Bran D.

-ANT: Glo, Alacia B.

-ANT: Glo, Alacia B.

-ANT: Glo, Alacia B.

-GANT: Gangolli, Esha A.

-green, Esha A.

-green, Esha A.

-green, Esha A.

-green, Sangolli, Sana A.

-green, Sangolli, Sana A.

-green, Printing Dare: 2003-03-10

-green Printing Dare: 2000-11-30

-green Printing Dare: 2000-11-30

-green Printing Dare: 2001-03-08

-green Printing Dare: 2001-13-08

-green Printing Dare: 2001-13-08

-green Printing Dare: 2001-10-05

-green Printing Dare: 2001-
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CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-1
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22392
LENGTH: 750
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Lepley, Denise M.
Rieger, Daniel K.
Burgess, Cathereine E.
Casman, Stacie, J.
Spytek, Kimberly A.
Boldog, Ferenc L.
                                                                                                                                                                                                                TYPE: PRT;
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-22392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-087-684-94; Sequence 94, Application US/10087684; bublication No. US20040029116A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 VHCSAGCGRTGV 238
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Sequence 7, Application US/09848294

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Sequence 7, Application US/09848294

Sequence 7, Application Oscillation Os
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Publication No. US20030113294A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TO FOCAL ADHESIONS AND USES THEREOF
FILE REFERENCE: 200125, 409C3
CURRENT APPLICATION NUMBER: US/10/293, 231
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 13
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100.0%; Pred. No. 0.072;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 11, Conservative
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; ORGANISM: Homo sapiens
US-10-293-231-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CONGANISM: Homosapiens
US-09-848-294-7
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Best Local Similarity
Matches 11; Conserva
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US-10-293-231-7
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APPLICANY: Anderson, David W.
APPLICANY: Miller, Charles E.
APPLICANY: Miller, Charles E.
APPLICANY: Gleev, Vadimir Y.
APPLICANY: Gleev, Vadimir Y.
APPLICANY: Gleev, Vadimir Y.
APPLICANY: Gleev, Vadimir Y.
APPLICANY: Purtak, Katarzyna
APPLICANY: Lepley, Denise M.
APPLICANY: Rieger, Daniel K.
APPLICANY: Rieger, Daniel K.
APPLICANY: Burgess, Catherine E.
TITLE OF INVENTION NOWBER: US/10/072,012
CURRENY PAPLICATION NOWBER: 60/265,102
PRIOR PELICATION NOWBER: 60/265,112
PRIOR APPLICATION NOWBER: 60/265,117
PRIOR APPLICATION NOWBER: 60/265,117
PRIOR APPLICATION NOWBER: 60/265,117
PRIOR APPLICATION NOWBER: 60/265,117
PRIOR APPLICATION NOWBER: 60/266,112
PRIOR APPLICATION NOWBER: 60/266,112
PRIOR APPLICATION NOWBER: 60/266,165
PRIOR APPLICATION NOWBER: 60/266,165
PRIOR APPLICATION NOWBER: 60/266,167
PRIOR P
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COTHER INFORMATION: Protein-tyrosine phosphatase Consensus Sequence
US-10-072-012-819
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100.0%; Pred. No. 0.07;
tive 0; Mismatches 0; Indels
                                            Sequence 819, Application US/10072012
Publication No. US20040033493A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   Gangolli, Esha
Padigaru, Muralidhara
Anderson, David W.
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                                                                                                                                                                                                                                                            Zerhusen, Bryan
Patturajan, Meera
Shimkets, Richard
                                                                                                                                                                        APPLICANT: Tchernev, Velizar APPLICANT: Spytek, Kimberly
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Best Local Similarity
Matches 11; Conserva
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Sequence 93, Application US/10087684; Publication No. US20040029116A1
GENERAL INFORMATION: APPLICANT: Edinger, Shlomit R.
4 KNRYKDVLPYD 14
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US-10-087-684-93
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11; Conservative 59 KNRYKDVLPYD 69 4 KNRYKDVLPYD 14

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| Patent No. US2002009762A1
| GENERAL INFORMATION:
| APPLICANT: Flint, Andrew J. APPLICANT: Coll, Deborah E. TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE TITLE OF INVENTION: PHOSPHATES
| TITLE OF INVENTION: PHOSPHATES | FILE REFERENCE: 200125.401 | CURRENT APPLICANTON NUMBER: US/09/788,626 | CURRENT FILING DATE: 2001-02-13 | NUMBER OF SEQ ID NOS: 40 | SOFTWARE: FastSEQ for Windows Version 4.0 | SEQ ID NO 22 | LENTH: 291
                                                                                                                                         Li, Li
Padigaru, Muralidhara
Mishra, Vishnu
Patturajan, Meera
Shenoy, Suresh
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Tchernev, Velizar
                         Casman, Stacie
Spytek, Kimberly
Boldog, Ferenc
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Malyankar, Uriel
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US-09-788-626-22
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US-10-218-779-93
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US-09-788-626-22
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Vernet, Corine A.M.
APPLICANT: Serbusen, Bryan D.
APPLICANT: Serbusen, Bryan D.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Malyankar, Uriel M.
APPLICANT: Miller, Charles E.
APPLICANT: Miller, Charles E.
APPLICANT: Miller, Charles E.
APPLICANT: Miller, Charles E.
APPLICANT: MILLER BRA A.
ITLER OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: 21402-214 CIP (CURRENT FILING DATE: 2003-03-10 PRIOR FILING DATE: 2000-11-29 PRIOR APPLICATION NUMBER: 60/254,180 PRIOR APPLICATION NUMBER: 60/264,180 PRIOR PLILNG DATE: 2001-01-25 PRIOR PLILNG DATE: 2001-03-08 PRIOR FILING DATE: 2001-03-08 PRIOR FILING DATE: 2001-03-08 PRIOR PLING DATE: 2001-03-08 PRIOR PLING DATE: 2001-05-05 PRIOR 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artifical Sequence: Domain US-10-087-684-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
2.4%; Score 11; DB 12; Length 263;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 11; Conservative 0; Mismatches 0; Indels
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                                                                                                        Stone, David J.
Grosse, William M.
Lepley, Denise M.
Rieger, Daniel K.
Burgess, Cathereine E.
Casman, Stacie, J.
Spytek, Kimberly A.
Boldog, Ferenc L.
                                                                                                                                                                                                                                                                                                                                                                                                                                          i, Li
adigaru, Muralidhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shenoy, Luca
Rastelli, Luca
Tchernev, Velizar T.
Vernet, Corine A.M.
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APPLICANT: MacDougall, John
APPLICANT: Millet, Isabelle
APPLICANT: Ellerman, Karen
APPLICANT: Stone, David
APPLICANT: Gerlach, Valerie
APPLICANT: Grosse, William
APPLICANT: Lepley, Denise
APPLICANT: Rieger, Daniel
MacDougall, John R.
Millet, Isabelle
Ellerman, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mishra, Vishnu
Shenoy, Suresh G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KNRYKDVLPYD 40
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US-10-218-779-93
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|||||||||||| 15 KARYKDVLPYD 25

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Search completed: August 17, 2004, 20:58:15 Job time : 47 secs

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

- protein search, using sw model OM protein

August 17, 2004, 20:49:12; Search time 16 Seconds (without alignments) 2753.482 Million cell updates/sec Run on:

US-10-087-993A-36

458 1 MSRSLDSARSFLERLEARGG.....NLRIGRPKGFRDPPAEWTRV 458 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

283366 segs, 96191526 residues Searched:

0 Word size : 283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description		-tyrosine-	protein-tyrosine-p	Yro	hypothetical prote	O.	. protein-tyrosine-p	tyrosine-	prot		hypothetical prote	protein-tyrosine-p	nbrane ty	recure	protein-tyrosine-p	leucocyte common a	probable protein-t	cyrosi	tyrosi	protein-tyrosine-p	tyrosi	e antige	eukocyte						
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	Length	750	303	802	913	928	1132	1187	18	248	340	340	382	582	597	694	773	775	780	0	딩	26	29	1437	49	49	20	ø	83	σ
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protein-tyrosine-preceptor tyrosine-protein-tyrosine-prot	protein-tyrosine-p protein-tyrosine-p protein-tyrosine-p protein-tyrosine-p protein-tyrosine-p
550893 130938 1495540 149354 568250 137577 137577 14871 148721 148721 148721	A57064 JC7503 T42636 B48148
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8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	4 4 4 4 4 5 6 4 5

# ALIGNMENTS

RESULT 1 S67100	
protein-tyrosine-phosphatase (EC 3.1.3.48) PTP2 - yeast (Saccharomyces cerevisiae)	
N,Alternate names: protein 04849; protein YOR208w	
C;Species: Saccharomyces cerevisiae	
C;Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text_change 21-Jul-2000	
C;Accession: S67100; A42667; A41980; S31554; S14170; JC1484; S42155	
R;Hughes, B.; Pohl, T.M.	
submitted to the Protein Sequence Database, July 1996	
A; Reference number: 866685	
A;Accession: S67100	
A;Molecule type: DNA	
A;Residues: 1-750 <hug></hug>	
A; Cross-references: EMBL: Z75116; NID: g1420486; PID: e2523394; PID: g1420487; MIPS: YOR208w	
A;Experimental source: strain S288C	
R; Guan, K.L.; Deschenes, R.J.; Dixon, J.E.	
J. Biol. Chem. 267, 10024-10030, 1992	
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J. Biol. Chem. 267, 10024-10030, 1992
A.Fitte: Isolation: and characterization of a second protein tyrosine phosphatase gene, PJ A.Riches. Isolation: and characterization of a second protein tyrosine phosphatase gene, PJ A.Accession: A42667; MUID:92250559; PMID:157774
A.Accession: A42667; MUID:92250559; PMID:157774
A.Molcule type: DNA
A.Richerence and MASSA
A.Accession: A41980
A.Accession: A41980
A.Accession: A41980; MUID:92196117; PMID:1549598
A.Accession: A1980; MUID:92196117; PMID:1549598
A.Accession: A1980; MUID:92196117; PMID:1549598
A.Accession: A1980; MUID:92196117; PMID:1549598
A.Accession: MUID:1919 Potein tyrosine phosphatase-encoding genes in the yeast Saccharr A.Reference number: S1554
A.Accession: S1554
A.Accession: S1554
A.Accession: S1554
A.Accession: S1554
A.Accession: S1470
A.Accession: S1410

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Mol. Cell. Biol. 12, 2396-2405, 1992
A; Title: Characterization of hematopoietic intracellular protein tyrosine phosphatases: c and threonine-rich sequences.
A; Reference number: A4430; MUID:92236615; PMID:1373816
A; Reference number: A4430; MUID:92236615; PMID:1373816
A; Molecule type: mRNA
A; Residues: 1-802 - 4MAID:
A; Residues: 1-802 - 4MAID:
A; Residues: 1-802 - 4MAID:
A; Coss.references: GB: M90388; NID:9200522; PIDN:AAA39994.1; PID:9200523
B; Cloutier, J.F.; Veillette, A.
EMBO J. 15, 4909-4918, 1996
A; Title: Association of inhibitory tyrosine protein kinase p50(csk) with protein tyrosine A; Reference number: S71952; MUID:97045099; PMID:8890164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Description: probably an effector and/or regulator of tyrosine protein kinase csk in T-C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 8; protein-tyrosine-phosphatase, ckeywords: phosphoprotein, phosphoria monoester hydrolase; tyrosine-specific phosphatase; F; 54-278/Domain: protein-tyrosine-phosphatase homology <PTP>
F; 497-802/Region: glutamic acid/proline/serine/threonine-rich
F; 613-621/Region: proline-rich
F; 688-695/Region: proline-rich
F; 227/Active site: Cys (phosphocysteine intermediate) #status predicted
F; 237/Active site: Substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: 441109
A;Molecule type: mRNA
A;Residues: 1-913 x'ANA
A;Cross-references: GB:M64572; NID:g179912; PIDN:AAA35647.1; PID:g179913
A;Cross-references: GB:M64572; NID:g179912; PIDN:AAA36647.1; PID:g179913
A;Cross-references: GB:M64572; NID:g179912; PIDN:AAA36647.1; PID:g179913
A;Title: Expression of cytoskeletal-associated protein tyrosine phosphatase PTPH1 mRNA ir A;Reference number: I55698; MUID:93179278; PMID:7874267
A;Accession: I55698
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A;Map position: 9431-9431
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF domain homology; pr
C;Superfamily: protein-tyrosine-phosphoric monoester hydrolase; tyrosine-specific phosphatase
F;31-308/Domain: protein 4.1 membrane-binding domain homology <B41>
F;516-590/Domain: GLGF domain homology <GLG>
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C;Date: 27-Mar-1992 #sequence_revision 02-May-1994 #text_change 21-Jun-2002
C;Accession: A41109; I55698
C;Accession: A41109; I55698
A;Yang, Q; Tonks, N.K.
Proc. Natl. Acad. Sci. U.S.A. 88, 5949-5953, 1991
A;Title: Isolation of a cDNA clone encoding a human protein-tyrosine phosphatase with hom A;Reference number: A41109; MUID:91296738; PMID:1648725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C, Complex: physically associates with inhibitory tyrosine protein kinase Csk; interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN3, nonreceptor type 3 [validated] - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 495-789 <CLO>C;Comment: This protein is found primarily in hematopoietic tissues.
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A;Molecule type: mRNA
A;Residues: 899-913 <RES>
A;Residues: 899-913 <RES>
A;Cross-references: GB:S76309; NID:g913165; PIDN:AAB33583.1; PID:g913166
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0
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100.0%; Pred. No. 0.027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
R; Matthews, R.J.; Bowne, D.B.; Flores, E.; Thomas, M.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 HCSAGCGRIGV 236
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Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: GDB:PTPN3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Function:
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                                                                                                                                                                                                                                                  A,Map position: 15R
C;Superfamily: protein-tyrosine-phosphatase homology
C;Reywords: cell division control; nucleotide binding; phosphoprotein; phosphoric monoes
F;469-676 Domain: protein-tyrosine-phosphatase homology <PTP>
F;669-674 /Region: nucleotide binding #status predicted
F;666/Active site: Cys (phosphocysteine intermediate) #status predicted
F;672/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein-tyrosine-phosphatase (BC 3.1.3.48), nonreceptor type pyp3 - fission yeast (Schiz
C,Species: Schizosaccharomyces pombe
C,Date: 10-8ep-1999 #sequence_revision 10-8ep-1999 #text_change 10-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Gene: pyp3
A Map position: 1
A introns 1
A introns 26/3
C isuperfamily: Schizosaccharomyces protein-tyrosine-phosphatase, nonreceptor type pyp3;
C isuperfamily: Schizosaccharomyces protein-tyrosine-phosphatase; tyrosine-specific phosphatase
C isuperfamily: protein-tyrosine-phosphatase homology of PTP>
F;227/Active site: Cys (phosphocysteine intermediate) #status predicted
F;237/Active site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:298595; PIDN:CAB11188.1; GSPDB:GN00066; SPDB:SPAC11E3.09
A;Experimental source: strain 972h-; cosmid c11E3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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R;Millar, J.B.A.; Lenaers, G.; Russell, P.
BMBO J. 11, 4933-4941, 1992
A;Title: Pyp3 PTPase acts as a mitotic inducer in fission yeast.
A;Reference number: $28392; WUID:93099868; PMID:1464318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.6%; Score 12; DB 2; Length 750;
100.0%; Pred. No. 0.0026;
vative 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.012;
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   A; Reference number: JC1484; MUID: 93083970; PMID: 1452018
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A;Molecule type: DNA
A;Residues: 1-303 <MUR>
                                                                              A;Molecule type: DNA
A;Residues: 1-370,'S',372-659,'GA',662-750 <JAW>
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                                                                                                                                            C;Genetics:
A;Gene: SGD:PTP2
A;Cross-references: SGD:S0005734; MIPS:YOR208w
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Matches 11; Conservative
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A;Accession: T37537
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-303 <MIL>
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                                       A;Accession: JC1484
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904 VHCSAGCGRTG 914

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Drotein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 14 - human NyAlternate names: PEZ protein-tyrosine-phosphatase/ezrin-like protein Cippecides: Homo sapiens (man) Cipate: 27-Aug-1995 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000 C;Accession: UC4155 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000 C;Accession: UC4155 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000 C;Accession: UC4155 #sex. Commun. 209, 959-965, 1995 A.i. Rogers, M.V.; Crompton, M.R. Biochem. Biochys. Res. Commun. 209, 959-965, 1995 A.i. Rogers, M.V.; Crompton, M.R. A;Accession: UC4155 #sex. MUID:95251727; PMID:7733990 A.i. Rogers, M.V.; Crompton, M.R. A;Accession: UC4155 #sex. MUID:95251727; PMID:7733990 A.i. Rogers = 11:187 *sex. A.i. Rog
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F.1121/Active site: Cys (phosphocysteine intermediate) #status predicted
F.1127/Binding site: substrate phosphate (Arg) #status predicted
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F:1123/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1129/Binding site: substrate phosphate (Arg) #status predicted
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100.0%; Pred. No. 0.038;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.038;
.ive 0; Mismatches 0; Indels
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hes 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           979 YIATQGPLPHT 989
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Best Local Similarity
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Matches
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S50578
hypothetical protein YER075c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 23-Mar-2001
C;Accession: S50578
R;Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae lambda clone 3612 and cosmid 9747.
A;Reference number: S50438
A;Molecule type: DNA
A;Residues: 1-928 <DIE>
A;Molecule type: DNA
A;Residues: 1-928 <DIE>
A;Genetics:
A;Genetics:
A;Genetics:
C;Genetics: SGD:S0000877; MIPS:YER075c
C;Genetics: SGD:S0000877; MIPS:YER075c
A;Map position: SR
C;Superfamily: protein-tyrosine-phosphatase homology
C;Keywords: phosphocyteine intermediate)
F;S27-867/Domain: protein-tyrosine-phosphatase homology
F;S27-867/Domain: protein-tyrosine-phosphates Hatatus predicted
F;810/Binding site: Substrate phosphate (Arg) #status predicted
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T49403
related to protein-tyrosine-phosphatase [imported] - Neurospora crassa
N;Alternate names: protein B1D4.180
C;Species: Neurospora crassa
C;Date: O'Date: O'Date
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F;670-890/Domain: protein-tyrosine-phosphatase homology <PTP>
F;842/Active site: Cys (phosphocysteine intermediate) #status predicted
F;848/Binding site: substrate phosphate (Arg) #status predicted
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100.0%; Pred. No. 0.037;
ive 0; Mismatches 0; Indels
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Pred. No. 0.031;
0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 11; Conservative 0; Mismatches 0; Indels
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2.4%; Score 11; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 11; Conservative 0; Mismatches
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Matches 11; Conservative
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A,Gene: F14023.24
A,Map position: 1
C,Superfamily: Dictyostelium protein-tyrosine-phosphatase, nonreceptor type 2; protein-ty
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R;Moriyama, T.; Kawanishi, S.; Inoue, T.; Imai, E.; Kaneko, T.; Xia, C.; Takenaka, M.; Nc
ESB Lett. 353, 305-308, 1994
A;Title: cDNA cloning of a cytosolic protein tyrosine phosphatase (RKPTP) from rat kidne,
A;Reference number: S48748; MUID:95046282; PMID:7957881
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Acsidues: 1-382 <MOR>
A;Cossidues: 1-382 <MOR>
A;Cossidues: 1-382 <MOR>
A;Crossidues: 1-382 <MOR
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 12; protein-tyrosine-phosphory
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F;58-282,Domain: protein-tyrosine-phosphatase homology <PTP>
F;231/Active site: Cys (phosphocysteine intermediate) #status predicted
F;231/Abinding site: substrate phosphate (Arg) #status predicted
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A)Residues: 1-582 <SCH>
A)Cross-references: GB:237988; NID:g993005; PIDN:CAA86070.1; PID:g993006
R;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
submitted to the EMBL Data Library, June 1993
A)Description: Assessment of the expression levels of murine protein-tyrosine phosphatase
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, B.Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.Accession: C96741
A.Accession: C96741
A.Status: preliminary
A.Molecule type: DNA
A.Molecul
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C;Species: Mus musculus (house mouse)
C;Accession: A57068; S40280
C;Accession: A57068; A20280
R;Schaapveld, R.Q.J.; van den Maagdenberg, A.M.J.M.; Schepens, J.T.G.; Olde Weghuis, D.;
R;Schaapveld, R.Q.J.; van den Maagdenberg, A.M.J.M.; Schepens, J.T.G.; Olde Weghuis, D.;
A;Title: The mouse gene Ptprf encoding the leukocyte common antigen-related molecule LAR:
A;Reference number: A57068; MUID:95394448; PMID:7665159
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C,Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
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N;Alternate names: leukocyte antigen-related protein LAR
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A;Noce: DKPZp761A0712.1
C;Superfamily: protein-tyrosine-phosphatase, receptor type N; protein-tyrosine-phosphata
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R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
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Plant Call 10, 849-87, 1998
A;Title: Molecular characterization of a tyrosine-specific protein phosphatase encoded
A;Reference number: 225483; MUID:98259006; PMID:9896642
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C,Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 02-Sep-2000
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
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100.0%; Pred. No. 0.13;
tive 0; Mismatches 0; Indels
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R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Weil, B.; Wiemann, S. submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Status: preliminary
A,Molecule type: mRNA
A,Molecule type: AAAA
A,Residues: 1-248 - AAAA
A,Cross-references: BMBL:All57451
A,Experimental source: adult amygdala; clone DKFZp761A0712
                                                                                                                                                                                                                              hypothetical protein DKFZp761A0712.1 - human (fragment)
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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A,Cross-references: EMBL:AF055635; PIDN:AAC68859.1
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Matches 10; Conservative
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A;Note: PTP1
C;Function:
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A; Experimental source: ovary

A; Experimental source: ovary

A; Mote: sequence extracted from NCBL backbone (NCBIN:149756, NCBIP:149758)

C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 9; cellular retinaldehyde-1

C; Superfamily: protein-tyrosine-phosphatase, noncester hydrolase; tyrosine-specific phosphatase; Keywords: phosphoprotein; monospecter hydrolase; tyrosine-specific phosphatase; F; 38-227/Domain: cellular retinaldehyde-binding protein homology <CRB>
F; 425-661/Domain: protein-tyrosine-phosphatase homology <PTP>
F; 4513/Active aite: Cys (phosphocysteine intermediate) #status predicted
F; 613/Binding site: substrate phosphate (Arg) #status predicted
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1, Biol. Chem. 269, 19645, 1994

A; Title: Characterization of two structurally related Xenopus laevis protein tyrosine phen type characterization of two structurally related Xenopus laevis protein tyrosine phen type characterization of two structurally related Xenopus laevis protein tyrosine phen type characterization of two structurally related Xenopus lassons B33978

A; Accession: B33978

A; Accession: B33978

A; Residues: 1-597 CDBL.

A; Resperimental source: Ovary

A; Note: sequence extracted from NCBI backbone (NCBIN:149759, NCBIP:149760)

C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 9; cellular retinaldehyde-c; Keywords: phosphotrein, phosphotre monoester hydrolase; tyrosine-specific phosphatas

C; Keywords: phosphoprotein, phosphory cannot be considered the considered by the c
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Biol. Chem. 269, 19639-19645, 1994
A;Title: Characterization of two structurally related Xenopus laevis protein tyrosine ph
A;Reference number: A53978; MUID:94308257; PMID:8034733
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 25-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                  C;Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane F;1-582/Domain: leukcoyte common antigen cytosolic domain homology (fragment) cLAC> F;0-271/Domain: protein-tyrosine-phosphatase homology *PTP1> F;339-562/Domain: protein-tyrosine-phosphatase homology *PTP2> F;232/Active site: Cys (phosphocysteine intermediate) #status predicted F;22/Anding site: Cys (phosphocysteine intermediate) #status predicted F;514/Active site: Cys (phosphocysteine intermediate) #status predicted F;514/Active site: cys (phosphocysteine intermediate) #status predicted F;520/Binding site: substrate phosphate (Arg) #status predicted
A,Accession: 840280
A,Molecule type: mRNA
A,Residues: 116-221 (HEN>
A,Cross-references: EMBL:Z23049; NID:g438135; PIDN:CAA80584.1; PID:g438136
G,Genetics:
A,Gene: Ptprf
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
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100.0%; Pred. No. 0.21;
tive 0; Mismatches 0; Indels
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A;Molecule type: mRNA
A;Residues: 1-694 <DEL>
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R;Del Vecchio, R.L.;
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RESULT 1
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1 MSRSLDSARSFLERLEARGG.....NLRIGRPKGPRDPPAEWTRV 458
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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PYP3 GCHPO
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### ALIGNMENTS

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Matches 12; Conservative
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P32587;
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MEDLINE=92196117; PubMed=1549598;
Ota I.M., Varshavsky A.;
"A gene encoding a putative tyrosine phosphatase suppresses lethality of an N-end rule-dependent mutant.",
Proc. Natl. Acad. Sci. U.S.A. 89:2355-2359(1992).
                                                                                                                              RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW
                                                                                                                                           RYKDVLPYDQTRVILSILQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW
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                                                                                                                                                                                                                                                                         TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQXRFLYHTVAQMFCSTLQNAS
                                                                                    1 MSRSIDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN
                                                                                                  1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN
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                                                                 Gaps
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales; Saccharomyces.
NCBI_TaxID=4932;
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  (BY
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Guan K., Deschenes R.J., Dixon J.E.;
"Isolation and characterization of a second protein tyrosine
phosphatase gene, PTP2, from Saccharomyces cerevisiae.";
J. Biol. Chem. 267:10024-10030(1992).
                                          Length 458;
PHOSPHOCYSTEINE INTERMEDIATE SIMILARITY). 46BCA1817C2C78B1 CRC64;
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [3]
SEQUENCE FROM N.A.
James P., Hall B.D., Whelen S., Craig B.A.;
Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases.
[4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
10-CCCT-2003 (Rel. 42, Last annotation update)
Procein-tyrosine phosphatase 2 (EC 3.1.3.48) (PTPase;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                kinase FUS3.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                 tyrosine + phosphate.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
SEQUENCE FROM N.A.

Hughes B., Pohl T.M.;

Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: May be implicated in the ubiquitin-mediated protein degradation pathway. May be involved in the regulation of MAP
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100.0%; Pred. No. 0.0013;
ve 0; Mismatches 0; Indels
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Millar J.B.A., Lenaers G., Russell P.;
"Pyp3 PTPase acts as a mitotic inducer in fission yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHOCYSTEINE INTERMEDIATE
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KL -> NV (IN REF. 1).
SP -> GA (IN REF. 3).
1033D2F0AA23BD35 CRC64;
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01-07T-1993 (Rel. 27, Last sequence update)
10-07T-2003 (Rel. 42, Last annotation update)
Protein-tyrosine phosphatase 3 (BC 3.1.3.48) (PTPase
PYP3 OR SPACIES.09
Schizosaccharomyces pombe (Fission yeast).
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Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
L -> S (IN REF.
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GG; GO05034; Cruncleus; IDA.
GG; GO0500387; Cruncleus; IDA.
InterPro; IPR000242; Tyr_PP.
Pfan; PR00102; Y_phosphatase; 1.
PRINTS; PR00700; PRTYPHPTASE.
SWART; SM00194; PTPc; 1.
PROSITE; PSS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PSS0055; TYR_PHOSPHATASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.0;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M85287; -; NOT ANNOTATED_CDS.

EMBL; M82872; AAA34922.1; -.

EMBL; M38723; AAB59323.1; -.

EMBL; Z75116; CAA99423.1; -.

PIR; S67100; S67100.

HSSP; P18052; IXFO.
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100.0%; Pred
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MOUSE
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                                               PTN8_MOUSE
ID PTN8_MOU
AC P29352;
                                                                            à
                                                                                  MEDIMINE-21948401; PubMed=11859360;

WEDIMINE-21948401; PubMed=11859360;

WOGOUTOG V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Squoros J., Peat N., Hayles J., Basham D., Bowaman S.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

A Brooks K., Gonnor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

A James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

Mooney P., Moule S., Mungall K., Murphy L., Nibhett D., Odell C.,

A James K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,

Rutherford K., Rutter S., Sauders R., Saare S., Stevens K.,

A Cliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,

Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Rodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Wolfjens I., Vanstreels E., Rieger M., Schaefer M., Mueller H., Pohl T.M.,

Bger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

Goffeau A., Cadleu E., Dreans S., Gloux S., Lelauc, Hurst S.M.,

Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

Bagar R.R., Cuzade L., Jimenez J., Sanchez M., del Rey F., Benito J.,

A Bagar R.R., Carlead L., Jimenez J., Sanchez M., del Rey F., Benito J.,

A Bagar R.R., Cuzade L., Jimenez J., Sanchez M., del Rey F., Benito J.,

A Bagar R.R., Cuzade L., Jimenez J., Armstrong J., Forsburg S.L.,

A Bagar R.R., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

A Shakovski G.V., Ussery D., Barrell B.G., Nurse P.,

Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tyrosine + phosphate.
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X69994; CAA49609.1; --
EMBL; X69994; CAA49609.1; --
PIR; S28392; S28392.
FASEP, P28827; IRPM.
GENEDB SPOWDE; SPACILE3.09; --
INTERPO; IPR000387; TYR_Phosphatase.
INTERPO; IPR000387; TYR_PP.
PR01012; Y_Phosphatase;
PRINTS; PR00102; Y_Phosphatase;
PRINTS; PR00104; PTPC; 1.
PROSITE; PS00983; TYR_PHOSPHATASE 1; 1.
PROSITE; PS00985; TYR_PHOSPHATASE 2; 1.
PROSITE; PS00985; TYR_PHOSPHATASE 2; 1.
PROSITE; PS0098; TYR_PHOSPHATASE 2; 1.
PROSITE; P
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EMBO J. 11:4933-4941 (1992).
                                               FROM N.A.
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92236615; PubMed=1373816;
MEDLINE=92236615; PubMed=1373816;
Matthews R.J., Bowne D.B., Flores E., Thomas M.L.;
Matthews R.J., Bowne D.B., Plores E., Thomas M.L.;
Characterization of hematepoletic intracellular protein tyrosine phosphatases: description of a phosphatase containing an SH2 domain and another enriched in proline-, glutamic acid-, serine-, and threonine-rich sequences "Mol. Cell. Biol. 12:2396-2405(1992).

Mol. Cell. Biol. 12:2396-2405(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosine + phosphate.
-!- SUBGELIULAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: Spleen, thymus, lympH node and bone marrow.
-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
                                                                                                                                                                                                                                                                                Eukaryotan, Mehazia, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Buthazia, Rodentia, Sciurognathi, Muridae, Murinae, Mus. NCBI TaxID=10090;
                                                                                                                                                               Protein-tyrosine phosphatase, non-receptor type 8 (EC 3.1.3.48) (Hematopoietic cell protein-tyrosine phosphatase 70Z-PEP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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PHOSPHOCYSTEINE INTERMEDIATE
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.4%; Score 11; DB 1; Length 802;
100.0%; Pred. No. 0.014;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0F1E45339BD4613E CRC64;
                                                            01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTNM_HUMAN STANDARD; PRT; 807 AA. 09Y2R7; 09563; 095064; 28-FEB-2003 (Rel. 41, Created) PFEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; B44390; B44390.

PDB; 1JEG; 31-OCT-01.

MGD; MGI:10770; PtpnB.

InterPro; IPR000242; TYR_Phosphatase.

InterPro; IPR000242; TYR_PP.

Pfam; PF00102; Y_PhosphaTase; 1.

PRINTS; SM00194; PTPC; 1.

PROSITE; PS000383; TYR_PHOSPHATASE_1; 1.

PROSITE; PS50055; TYR_PHOSPHATASE_2; 1.

PROSITE; PS50055; TYR_PHOSPHATASE_2; 1.

PROSITE; PS50055; TYR_PHOSPHATASE_2; 1.

PAGFIRE; PS50055; TYR_PHOSPHATASE_2; 1.

PAGFIRE; PS50055; TYR_PHOSPHATASE_2; 1.
802 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M90388; AAA39994.1; -.
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Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 HCSAGCGRIGV 238
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                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
PINM HUMAN
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Gaps

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                                                                                                                                                                  MEDIJINE-99168989; PubMed-10068674; Cohen S., Dadi H., Shaoul E., Sharfe N., Roifman C.M.; Cohen S., Dadi H., Shaoul E., Sharfe N., Roifman C.M.; Cohen S., Dadi H., Shaoul E., Sharfe N., Roifman C.M.; Cohen S., Dadi H., Shaoul E., Sharfe N., Roifman C.M.; Inducible human processine phosphatase, Lyp."; Blood 93:2013-2024 (1999).
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).

Liu T., Zhang J., Fu G., Zhang Q., Ye M., Zhou J., Wu J., Shen Y.,

Yu M., Chen S., Mao M., Chen Z.;

Yu M., Chen S., Mao M., Chen Z.;

Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

-!- FUNCTION: Seems to act on Cbl. May play a role in regulating the
function of Cbl and its associated protein kinases.

-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
                                                                                                                                                                                                                                                                                                                                                                                                                          tyrosine + phosphate.
-! SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- ALTERNATIVE PRODUCTS:
EVENT_ALTERNATIVE PRODUCTS:
EVENT_ALTERNATIVE SPLICING; Named isoforms=2;
Name=1; Synonyms=LyP1;
Isold=09VSR2-1; Sequence=Displayed;
Name=2; Synonyms=LyP2;
Isold=09VSR2-2; Sequence=VSP 005134;
-!- TISSUE SPECIFICITY: Predominantly expressed in lymphoid tissues and cells Isoform 1 is expressed in thymocytes and both mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the protein-tyrosine phosphatase family. Non-receptor class subfamily.
                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS, PROJUCTO, PRTYPHPHTASE.
SMART; SMO0194, PTPC; 1.
PROSTIE; PSO0389, TYR PHOSPHATASE.1; 1.
PROSTIE; PSSO056, TYR PHOSPHATASE.2; 1.
PROSTIE; PSSO056, TYR PHOSPHATASE.PTP; 1.
Hydrolase; Alternative splicing.
DOMAIN 23 288 PROTEIN-TYROSINE PHOSPHATASE.
ACT_SITE 227 227 SIMILARITY).
                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> GKWFSWL (in isoform 2).

/FIId-VSP 005134.

KP -> NA (IN REF. 1).

V -> G (IN REF. 2).

G -> V (IN REF. 2).

I -> IV (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 600716; -.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_PP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AF001846; AAD00904.1; -. EMBL; AF001847; AAD00905.1; -. EMBL; AF077031; AAD27764.1; -. HSSP; P29350; IGWZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:9652; PTPN22.
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126
147
240
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                                                                                                                       WCBI_TaxID=9606;
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147
240
                                                    TPN22 OR PTPN8
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CONFLICT
CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB=Colon;
MEDLINE=29327504; PubMed=1626183;
MEDLINE=29327504; PubMed=1626183;
Arimura P.Y., Hinoda Y., Itoh F., Takekawa M., Tsujisaki M., Adachi M.,
Imai K., Yachi A.;
"CDNA cloning of new protein tyrosine phosphatases in the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytoskeleton.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein tyrosine + phosphate + CATALYTIC ACTIVITY: Protein tyrosine + phosphates + COATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
-!- SIMILARITY: Contains 1 FERM domain.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Expression of cytoskeletal-associated protein tyrosine phosphatase PTPH1 mRNA in human hepatocallular carcinoma.";
J. destroenterol. 29:727-732(1994).
-i- FUNCTION: May act at junctions between the membrane and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDILINE-91296738, PubMed=1648725;
Yang O., Tonks N.K.;

"Isolation of a cDNA clone encoding a human protein-tyrosine
phosphatase with homology to the cytoskeletal-associated proteins
band 4.1, ezrin, and talin.",
Proc. Natl. Acad. Sci. U.S.A. 88:5949-5953(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 889-913 FROM N.A.
MEDLINE=95179278; PubMed=7874267;
Ikuta S., Itoh F., Hinoda Y., Toyota M., Makiguchi Y., Imai K.,
Yachi A.;
                                                                                                                                                                                                                                                                                                                                                    01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
10-CT-2003 (Rel. 42, Last annotation update)
Protein tyrosine phosphatase, non-receptor type 3 (EC 3.1.3.48)
PROTEIN-tyrosine phosphatase H1) (PTP-H1).
                                                                                                                                          .
0
                                                                                               2.4%; Score 11; DB 1; Length 807; 100.0%; Pred. No. 0.014;
                                                                                                                                          0; Indels
420 420 L -> P (IN REF. 2).
620 620 R -> W (IN REF. 2).
742 P -> S (IN REF. 2).
807 AA; 91704 MW; IABERBAE89C9D9FBF CRC64;
                                                                                                                                                                                                                                                                                                                          913 AA
                                                                                                                100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         colon.";
Tumour Biol. 13:180-186(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 194-896 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M64572; AAA35647.1; -.
EMBL; S39392; AAB22439.2; -.
                                                                                                                       Local Similarity 100.
1es 11; Conservative
                                                                                                                                                                                  228 HCSAGCGRTGV 238
                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                          226 HCSAGCGRTGV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                        PIN3 HUMAN
P26045;
  CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                           PTN3_HUMAN
                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                      RESULT 6
                                                                                                                                                                                      ઠ
                                                                                                                                                                                                                                                                                                                              ELHORSSPPPLPERTLESPFLADEDCMQAQSIETYSTSY
PDIMENSTSSKQTLKTPGKSPTRSKSLKILRNMKKSICNSC
PPNKPAESVQSNNSSSPLNFGFANRFSKPKGPRNPPPTWNI
      Protein-tyrosine phosphatase, non-receptor type 22 (EC 3.1.3.48) (Hematopoietic cell protein-tyrosine phosphatase 702-PEP) (Lymphoid phosphatase) (LyP).
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Hydrolase.
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ACT_SITE
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Matches
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SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
MEDLINE=37313264; PubMed=9169868;
Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,
Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
Hunicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
EMBL; S76309; AABJ3320...,

R PIR; A41109; A41109.

DR Genew; HGNC:9655; PTPN3.

DR GO: GO:0004725; F:protein tyrosine phosphatase activity; TAS.

DR GO; GO:0004725; F:protein amino acid dephosphorylation; TAS.

DR GO; GO:0004725; F:protein amino acid dephosphorylation; TAS.

DR GO; GO:0004725; F:protein amino acid dephosphorylation; TAS.

DR InterPro; IPR001478; PDZ.

DR InterPro; IPR001478; PDZ.

DR InterPro; IPR00142; TYR Ph.

DR Pfam; PF001021; TYR Ph.

DR Pfam; PF001021; TYR Ph.

DR PFNNTS; PR00105; PDZ; 1.

DR PRNTS; PR00105; PR1YPHPHTASE.

DR PRNTS; PR00105; PTPC; 1.

DR SWART; SW00228; PDZ; 1.

DR SWART; SW00124; PTPC; 1.

DR SWART; PS00106; PERM 1; 1.

DR PROSITE; PS00106; PERM 1; 1.

DR PROSITE; PS00106; PERM 2; 1.

DR PROSITE; PS00106; TRR PHOSPHATASE 1; 1.

DR PROSITE; PS00105; TYR PHOSPHATASE 1; 1.

THOM THE TYR PHOSPHATASE 1; 1.

THE TYR PHOSPHATASE 1; 1.

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01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein-tyrosine phosphatase 3 (EC 3.1.3.48) (PTPase 3).
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales; Saccharomycetacee; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE-97367951; Pubmed-9224718;
Zhan X.-L., Deschenes R.J., Guan K.-L.,
"Differential regulation of FUS3 MAP kinase by tyrosine-specific phosphatases PTP2/PTP3 and dual-specificity phosphatase MSG5 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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PHOSPHOCYSTEINE INTERMEDIATE
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29A539ACDE2F1515 CRC64;
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Genes Dev. 11:1690-1702(1997).
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PTP3 YEAST
ID PTP3 YEAST
 P40048;
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ACT_SITE
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Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";

Nature 387:78-81(1997).

-! FUNCTION: Major phosphatese responsible for tyrosine dephosphorylation of MaP kinase FUS3 to inactivate its activity; it also has important roles, along with MSG5, in the inactivation of FUS3 following pheromone stimulation.

-! CATALVITY: Palongs pheromone stimulation.

-! CATALVITY: Balongs to the protein-tyrosine phosphate + H(2)O = protein tyrosine + phosphate.

-! SIMILARTIY: Balongs to the protein-tyrosine phosphatase family.

-! SIMILARTIY: Contains 1 rhodanese domain.
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ID PTINE_HUMAN

C15678,

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOY-2003 (Rel. 42, Last annotation update)

DT 00-CCT-2003 (Rel. 42, Last annotation update)

DT 10-CCT-2003 (Rel. 42, Last annotation update)

DE Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)

DE (Protein-tyrosine phosphatase pez).
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PHOSPHOCYSTEINE INTERMEDIATE (BY
SIMILARITY).
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100.0%; Pred. No. 0.016;
cive 0; Mismatches 0; Indels
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592 597 POLY-THR.
724 715 POLY-ASD.
724 732 POLY-ASP.
928 AA, 105250 MW; 6DECSBA26B7ACBCB CRC64;
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nes 11; Conservative
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Thu Aug 19 09:28:45 2004

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

PTPN14 OR PEZ. Homo sapiens (Human)

NCBI\_TaxID=9606;

Length 1187; Score 11; DB 1; Length 118 Pred. No. 0.019; 0; Mismatches 0; Indels Query Match 2.4%; Best Local Similarity 100.0%; Matches 11; Conservative 0 101 YIATQGPLPHT 111

979 YIATQGPLPHT 989 RESULT 9

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PRT; 1189 AA.

STANDARD;

PTNE\_MOUSE ID PTNE\_MOUSE

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; 0

Indels

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0; Mismatches

100.0%;

Local Similarity 100 nes 11; Conservative 101 YIATQGPLPHT 111 981 YIATQGPLPHT 991

Best Loca Matches

à g

Query Match

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Gaps

0

Blochem. Bloches. Eds. Commun. 209:959-965(1995).

-!-CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.

-!-TISSUB SPECIFICITY: Expressed in a variety of human tissues including kidney, skeletal muscle, lung and placenta.

-!-SIMILARITY: Contains I FERM domain.

-!-SIMILARITY: Contains to the protein-tyrosine phosphatase family.

Non-receptor class subfamily. TISSUE=Breast carcinoma; MEDLINE=92251727; PubMed=7733990; MEDLINE=92251727; PubMed=7733990; Smith A.L., Mitchell P.J., Shipley J., Gusterson B.A., Rogers M.V., Crompton M.R.; Crompton M.R.; a novel human cDNA encoding protein tyrosine phosphatase- and (BY SIMILARITY) POLY-PRO. EMBL; X82676; CAA57993.1; -. PIR; JC4155; JC4155. HSSP; P29350; 1GWZ. Genew; HGNC:9647; PTPN14. "Pez: a novel human clezrin-like domains."; SEQUENCE FROM N.A. DOMAIN SEQUENCE ACT\_SITE DOMAIN 

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"cDNA cloning of a novel protein tyrosine phosphatase with homology
to cytoskeletal protein 4.1 and its expression in T-lineage cells.";
Biochem. Biophys. Res Commun. 203.479-484(1994)
-i. FUNCTION: MAY BE INVOLVED IN THE REGULATION OF T CELL DEVELOPMENT.
-i. CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein non-hematopoietic origins.
-!- SIMILARITY: Contains 1 FERM domain.
-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily. tyrosine + phosphate. -!- TISSUE SPECIFICITY: Thymus; in cells of both hematopoietic and Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)
(Protein-tyrosine phosphatase PTP36). 2.4%; Score 11; DB 1; Length 1189; 100.0%; Pred. No. 0.019; PROTEIN-TYROSINE PHOSPHATASE PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY). 1189 AA; 135030 MW; 2B85BE5F9C723303 CRC64; SMAKI, SWOLLT, ELEM 1: 1.

PROSITE; PS00661; FERM 1: 1.

PROSITE; PS00661; FERM 2: 1.

PROSITE; PS001831; TYR PHOSPHATASE 1: 1.

PROSITE; PS50055; TYR PHOSPHATASE PTP: 1.

PROSITE; PS50056; TYR PHOSPHATASE PTP: 1.

Structural protein; Cytoskeleton; Hydrolase. POLY-PRO. POLY-GLY. POLY-GLU PIR; JC2366; JC2366. HSSP; Q06124; ZSHP. MGD; MGI:102467; Fupul4. InterPro; IPR000299; Band 4.1. InterPro; IPR000387; TYR\_phosphatase. InterPro; IPR000242; TYr\_PP. FERM. SEQUENCE FROM N.A. STRAIN-CB-17-SCID; TISSUE-Thymus; MEDLINE-94354845; PubMed-8074693; Pfam, PF00373; Band 41; 1.
Pfam, PF00102; Y\_phosphatase; 1.
PRINTS; PR00935; BAND41.
PRINTS; PR00700; PRTYPHPHTASE.
SWART; SM00295; B41; 1.
SWART; SM00194; PTPC; 1. EMBL; D31842; BAA06628.1; -. Mus musculus (Mouse) NCBI\_TaxID=10090; DOMAIN ACT\_SITE SEQUENCE DOMAIN DOMAIN STATE THE TENT TO BE THE TENT TO THE TENT

775 AA; 86992 MW; 7106D73F5014E411 CRC64;

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SEQUENCE
                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=BALB/c;
MEDLINE=95289971; PubMed=7772023;
Charest A., Wagner J., Shen S.H., Tremblay M.L.;
"Murine protein tyrosine phosphatase-PEST, a stable cytosolic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tyrosine phosphatase.";
Biochem. J. 308:425-432(1995).
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tyrosine + phosphate.
-!- SUBCELULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS TO 297-416.
MEDLINE-53112015; PubMed=1472029;
MEDLINE-53112015; PubMed=1472029;
MEDLINE-53112015; PubMed=1472029;
Adachi M., Ital K., Yachi A.;
Adachi M., Imai K., Yachi A.;
"Cloning and characterization of a human cDNA encoding a novel
                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus.
NCBI_TaxID=10090;
                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Frotein-tyrosine phosphatase, non-receptor type 12 (EC 3.1.3.48)
Protein-tyrosine phosphatase P19) (P19-PTP) (MPTP-PEST).
PTPN12.
                                                                                                                                                                                                                                                                                                                                                                MEDINE-92272714; PubMed-1590786; den Hertog J., Pals C.E., Jonk L.J., Kruijer W.; lulfferential expression of a novel murine non-receptor protein tyrosine phosphatase during differentiation of P19 embryonal carcinoma cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY
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PHOSPHOCYSTEINE INTERMEDIATE (B SIMILARITY).
K -> N (IN REF. 1).
KQDSP -> DETS (IN REF. 1).
W -> V (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 putative cytoplasmic protein-tyrosine-phosphatase.";
Biochem. Biophys. Res. Commun. 189:1223-1230(1992).
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EMBL; X86781; CAA60477.1; -.
PIR; S55345; S55345.
HSSP; QG0124; 2SFP.
MGD; MGI:104673; Ptpn12.
INTERPO: IPR000387; TYR_Phosphatase.
INTERPO: IPR000242; TYT_PP.
PERMYS; PR00102; Y phosphatase; I.
PRINTS; PR00104; PTP: 1.
PROSITE; PS00194; PTP: 1.
PROSITE; PS00184; PTP: 1.
PROSITE; PS00185; TYR_PHOSPHATASE_1; I.
PROSITE; PS50056; TYR_PHOSPHATASE_2; I.
PROSITE; PS50056; TYR_PHOSPHATASE_2; I.
                                                              775 AA.
                                                              STANDARD;
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328
380
                                                           PINC MOUSE
P35831;
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"Chromosomal localization of the protein tyrosine phosphatase G1 gene "Chromosomal localization of the aberrant transcripts in human colon cancer cells.";
FEBS Lett. 339:1222-228 (1994).
-!- CATALYTIC ACITVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.
-!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- DISEASE: DEFECTS IN PTPN12 ARE FOUND IN SOME COLON CANCERS.
-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=93203562; PubMed=8454633;
Yang Q.C., Torks N.K., Sommercorn J.;
"Cloning and expression of PPP-PEST. A novel, human, nontransmembrane, protein tyrosine phosphatase.";
J. Biol. Chem. 268:6622-6628(1993).
                                                                  Gaps
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MEDLINE-94156037; PubMed=7509295;
Takekawa M., Itoh F., Hinoda Y., Adachi M., Ariyama T., Inazawa J.,
Imai K., Yachi A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Σ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                            PINC HUMAN STANDARD, PRT, 780 AA.
005209; 016130;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 42, Last annotation update)
Fordein-tyrosine phosphatase, non-receptor type 12 (EC 3.1.3.48)
Protein-tyrosine phosphatase G1) (PTPG1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Colon;
MEDLINE=93112015; PubMed=1472029;
MEDLINE=93112016; PubMed=1472029;
Adachi M., Iroh F., Hinoda Y., Arimura Y., Toyota M., Sekiya Adachi M., Imai K., Yachi A.;
Adachi M., Imai K., Yachi A.;
"Cloning and characterization of a human cDNA encoding a novel putative cytoplasmic protein-tyrosine-phosphatase.";
Biochem. Biophys. Res. Commun. 189:1223-1230(1992).
                                                                     .
2.2%; Score 10; DB 1; Length 775;
100.0%; Pred. No. 0.13;
ive 0; Mismatches 0; Indels
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Genew; H9MC:9645; PTPN12.
MIM; 600079; --
GO; GO:0005737; C:Cytoplasm; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, D13380; BAA02648.1; -. EMBL; M93425; AAA36529.1; -. EMBL; S69184; AAB30047.2; -. PIR; JC1368; JC1368.
                                 Local Similarity 100.
nes 10; Conservative
                                                                                                                                        228 HCSAGCGRTG 237
                                                                                                                                                                                                          230 HCSAGCGRTG 239
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PINC_HUMAN
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Name=2; Synonyms=Type 2-PTP-NP;

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                            protein tyrosine phos. . .; TAS.
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PROSEG; 003134; P70328;
00.1-NOV-1997 (Rel. 35, Last sequence update)
10.0CT-2003 (Rel. 42, Last annotation 
10.0CT-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification of a second transmembrane protein tyrosine phosphatase, IA-2beta, as an autoantigen in insulin-dependent diabetes mellitus: precursor of the 37-kpa tryptic fragment."; Proc. Natl. Acad. Sci. U.S.A. 93:2307-2311(1996).
-!- FUNCTION: Implicated in development of nervous system and pancreatic endocrine cells.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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TISSUE-Meonatal brain;
MISDLINE-96197307; PubMed-8637868;
Lu J., Li Q., Xie H., Chen Z.-J., Borovitskaya A.E., Maclaren N.K.,
Notkins A.L., Lan M.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ICR; TISSUE=brain; MEDLINE=96281667; PubMed=8681804; Achiang M.-K., Flanagan J.G.; "PTP-NP, a new member of the receptor protein tyrosine phosphatase family, implicated in development of nervous system and pancreatic endocrine cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
GO; GO:0005625; C:soluble fraction; TAS.
GO; GO:0004726; F:non-membrane spanning protein tyrosine phos.
GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
InterPro; IPRO00342; TYR phosphatase.
InterPro; IPRO00342; Tyr PP.
FEAM; PF00102; Y phosphatase; 1.
RINTS; PR00102; Y phosphatase; 1.
RRINTS; PR00104; PTC; 1.
RRNT; SM00194; PTC; 1.
RROSITE; PS000383; TYR PHOSPHATASE 1; 1.
RROSITE; PS50056; TYR PHOSPHATASE 2; 1.
RROSITE; PS50055; TYR PHOSPHATASE PTP; 1.
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                                                                                                                                                                                                                                                                            PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).

K -> R (in colon cancer).
/FIId=VAR 006385.
V -> I (IN REF. 2).
V -> I (IN REF. 2).
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-!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.2%; Score 10; DB 1; Length 780;
100.0%; Pred. No. 0.13;
                                                                                                                                                                                                                                                        PROTEIN-TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         48F7EE5FDAEF7512 CRC64;
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Comment-Additional isoforms seem to exist,
Name=1; Synonyms-Type 1-PTP-NP;
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                                                                                                                                                                                                                                                                                                                                                                                                           88092 MW;
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Best Local Similarity 100.
Matches 10; Conservative
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780 AA;
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PTPX MOUSE
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Isoldablobase in the state of the state of pancreatic lesses of pancreas and brain.

-1-TISSUE SPECIFICITY: Pancreas and brain.
-1-DEVELOPMENTAL STRAGE: Expressed in day 8.5 embryos (EB.5) in the development. First expressed in day 8.5 embryos (EB.5) in the dorsal part of the midgut endoderm and by E9.5, in the pancreatic rudiment specifically in early endocrine progenitor cells. It later stages expressed in insulin- or glucagon-producing cells. During neural development, the type 2 PTP-NP is expressed in early stages of neurogenesis, and the type 1 weakly in the later stages.
-1-PTM: Appears to undergo multiple proteolytic cleavage at consecutive basic residues (By similarity).
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PROTEIN-TYROSINE PHOSPHATASE.
PHOSPHOCYSTEINE INTERMEDIATE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last unnotation update)
Receptor-type protein-tyrosine phosphatase N2 precursor (EC 3.1.3.48)
(R-PTP-N2) (PTP NE-6) (PTPNE6) (Phogrin).
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MGD, MGILOU418, PUPIN2.

RILCEPEO, IPRO00242; TYR_Phosphatase.

InterPro; IPRO00242; TYR_Phosphatase.

RILCEPEO, IPRO00102; Y_phosphatase.

REAM, PRO010102; Y_phosphatase.

REAM, PRO010102; Y_phosphatase.

REAM, PRO010102; Y_phosphatase.

REAM, PRO010102; Y_phosphatase.

REAM, PRO01102; PRO0102; TYR_PHOSPHATASE.

REAM, PROSITE; PS50055; TY
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550 N-LINKED (GLCNAC. . .) (POTENTIN MISSING (IN REF. 2).
411 I -> P (IN REF. 2).
411 S -> L (IN REF. 2).
596 L -> H (IN REF. 2).
5111554 MW; 6B73EACA535D2BE5 CRC64;
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100.0%; Pred. No. 0.17;
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EMBL; U82439; AAB3996.1; -.
HSSP; P18052; 1YFO.
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1001 AA;
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Q63475;
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                                                                                                                                                  TISSUB-Pancreatic islets;

MEDLINE-97254813; PubMed=9100223;

MEDLINE-97254813; PubMed=9100223;

MEDLINE-97254813; PubMed=9100223;

Sheppard P., Kindsvogel W., Hagopian W.A.;

Sheppard P., Kindsvogel W., Hagopian W.A.;

"An islet-cell protein tyrosine phosphatese is a likely precursor to the 37-kba autoantigen in type I diabetes: human and macaque predictive autoantibodies.";

Mol. Med. 3:163-1731(1997).

-!- FUNCTION: Implicated in development of nervous system and pancreatic endocrine cells.

-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
Receptor-type protein-tyrosine phosphatase N2 precursor (EC 3.1.3.48) (R-PTP-N2) (M1851).
                                                                                                                                                                                                                                                                                                                                                                         tyrosine + phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
-!- TISSUE SPECIFICITY: Brain, prostate, pancreatic islets. Lower expression in spinal cord, thyroid, adrenal medulla and gastrointestinal tract.
                                                  Macaca nemestrina (Pig-tailed macaque).
Bukaryota: Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- PTM: Appears to undergo multiple proteclytic cleavage at consecutive basic residues (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U91574; AAC51186.1; -. HSSP; P18052; 1YFO.
                                                                                                                       NCBI_TaxID=9545;
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CLEAVAGE SITE (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
                  Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                     STRAIN=Sprague-Dawley,
Fitzgerald L.R., Walton K.M., Dixon J.E., Largent B.L.;
Submitted (Nov-1996) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: Implicated in development of nervous system and
pancreatic endocrine cells.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
-!- tyrosine + phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
-!- TISSUE SPECIFICITY: Pancreas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                           -i- PTM: Appears to undergo multiple proteolytic cleavage at consecutive basic residues (By similarity).
-i- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.2%; Score 10; DB 1; Length 1004; 100.0%; Pred. No. 0.17; 0; Indels ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P18054; 1170.
InterPro; 1R0003037; TYR phosphatase.
InterPro; PR000242; Tyr PP.
Pfam; PF00102; Y phosphatase; 1.
PRINTS; PR00100; PRTYPHPHTASE.
SMART; SM001194; PPPC; 1.
PROSITE; PS00383; TYR PHOSPHATASE 1; 1.
PROSITE; PS0055; TYR PHOSPHATASE 2; 1.
PROSITE; PS0055; TYR PHOSPHATASE PPP; 1.
Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane.
SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
PROTEIN-TYROSINE PHOSPHATASE.
                                                                                                     SEQUENCE FROM N.A. STRAIN-New England Deaconess Hospital; TISSUE=Insulinoma; Wasmeler C., Hutton J.C.; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111863 MW; A73929E11B486FB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z50735; CAA90600.1; -.
EMBL; U73458; AAC08036.1; -.
HSSP; P18052; 1YFO.
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553 55
1004 AA;
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                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58
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Best Local S
Matches 10
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DOMAIN
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0
InterPro; IPR001243; TYR phosphatase.
InterPro; IPR001242; TYr PP.
Pfam, PF00102; Y_phosphatase.
InterPro; IPR001242; TYr PP.
Promine; PR00109; Y_phosphatase.
SMART; SM01194; PTPc; 1.
PR051TE; PS001383; TYR PHOSPHATASE 1; 1.
PR051TE; PS50055; TYR PHOSPHATASE 2; 1.
PR051TE; PS50055; TYR PHOSPHATASE 2; 1.
PR051TE; PS50055; TYR PHOSPHATASE 2; 1.
PR051TE; PS50055; TYR PHOSPHATASE PTP; 1.
PR051TE; PS50055; TYR PHOSPHATASE TYP; 1.
PR051TE; PS50055; TYR PHOSPHATASE TYP: 1.
PR051TE; PS50055; TYR PHOSPHATASE TYPE TYPE ROTEIN-TYROSINE CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.2%; Score 10; DB 1; Length 1013; 100.0%; Pred. No. 0.17; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                  PROTEIN-TYROSINE PHOSPHATASE. PHOSPHOCYSTEINE INTERMEDIATE
                                                                                                                                                                                                                                                                                                                                                                                              CLEAVAGE SITE (BY SIMILARITY)
N-LINKED (GLCNAC. . .) (POTEN
                                                                                                                                                                                                                                                                                                                                                                                                                               1013 AA; 111190 MW; 4808D43937A2EF59 CRC64;
                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                            PHOSPHATASE NZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 10; Conservative
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634
1013
1002
943
426
562
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PTPX_HUMAN
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Created) Last sequence update) Last annotation update)

(Rel. 35, (Rel. 35, (Rel. 42,

01-NOV-1997 01-NOV-1997 10-OCT-2003

DATA DATA DATA

STANDARD;

\_PTPX\_MACNE 002695;

RESULT 14 PTPX\_MACNE

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MEDINE-2238257; PubMed=12477932;

MEDINE-2238257; PubMed=12477932;

MISURE-2238257; PubMed=12477932;

MISURE-2238257; PubMed=12477932;

MISCHII S.F., Zeeberg B.L., Marchan F.S., Mannen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Mischin S.F., Zeeberg B. B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Mischin S.F., Zeeberg B. B., Berers G.J., Mann J., Hsieh F.,

Brownstein M., Soares M.B., Bonaldo M.F., Carning D., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carningi P., Prange C.,

Raha S.S., McKwan P.J., McKernan K.J., Malek J.A., Guntarane P.H.,

Rabask S.A., McKwan P.J., McKernan K.J., Malek J.J., Hulyk S.W.,

Milalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Mhiting M., Madan A., Young A.C., Shewchenko Y., Buffard G.G.,

Mhiting M., Madan A., Young A.C., Schamuz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

Human and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-1690312002).

"In Chraktic Activity: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Fetal brain;
MEDLINE=97127415; PubMed=8954911;
Smith P.D., Barker K.T., Wang J., Lu Y.-J., Shipley J., Crompton M.R.;
"ICAAR, a novel member of a new family of transmembrane, tyrosine
phosphatase-like proteins.";
Biochem. Biophys. Res. Commun. 229:402-411(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cui L., Yu W.-P., de Airpurua H.J., Schmidli R.S., Pallen C.J.; "Cloning and characterization of islet cell antigen-related protein-tyrosine phosphatass (PTP), a novel receptor-like PTP and autoantigen in insulin-dependent diabetes."; J. Biol. Chem. 271:24817-24823(1996).
PIPX_HUMAN STANDARD; PRT; 1015 AA.
092923; 08NHS; 092662;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
(Rel. 42, Last annotation update)
(Re-CEPLOR) (Rel. 42, Last annotation update)
(Re-PPLOR) (Islet cell autoantigen related protein) (ICAAR) (IAR)
                                                                                                                                                                                                                                                                                                                      TISSUE=Pancreas;
MEDLINE=Pancreas;
MEDLINE=Pancreas;
Kawasaki E., Hutton J.C., Eisenbarth G.S.;
Kawasaki E., Hutton J.C., Eisenbarth G.S.;
Molecular cloning and characterization of the human transmembrane
Molecular cloning and characterization of the human transmembrane
protein tyrosine phosphatase homologue, phogrin, an autoantigen of
type 1 diabetes.";
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tyrosine + phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Brain, and Pancreas;
MEDLINE=96394649; PubMed=8798755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                    (Phogrin).
                                                                                                                                                                             PTPRN2
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Event=Alternative splicing; Named isoforms=2;

Name=1; Isoid=Q92932-1; Sequence=Displayed;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 601698; -.

R GO; GO:0005887; C:integral to plasma membrane; TAS.

R GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. .;

R GO; GO:0006470; F:transmembrane acid dephosphorylation; TAS.

R InterPro; IPR00355; PTPc motif.

R InterPro; IPR00337; TYP phosphatase.

R InterPro; IPR000243; TYP phosphatase.

R PRINTS; PR00700; PRTYPHHTASE.

R SWART; SM00104; PTPc, motif; 1.

DR RART; SM00104; PTPc, motif; 1.

DR ROSITE; PS00383; TYR PHOSPHATASE 2; 1.

DR PROSITE; PS50056; TYR PHOSPHATASE 2; 1.

DR PROSITE; PS50055; TYR PHOSPHATASE 2; 1.

DR PROSITE; PS50055; TYR PHOSPHATASE 2; 1.

R Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane; My diabetes mellitus; Alternative splicing.

FT CHAIN 22 1015 PHOSPHATASE.

PHOSPHATASE PROFENTARE.

PHOSPHATASE
                                          Lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                 -!- MISCELLANEOUS: Optimum activity is measured at pH 4.5.
-!- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.
                                                                                                                                                                      -!- DISEASE: Autoantigen in insulin-dependent diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
       Note=No experimental confirmation available:
-!- TISSUE SPECIFICITY: Highest levels in brain and pancreas.
-!- DOMAIN: The cytoplasmic domain appears to contain the autoantigenic epitopes.
-!- PTM: Appears to undergo multiple proteolytic cleavage at consecutive basic residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHOCYSTEINE INTERMEDIATE (BY
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554 N-LINKED (GLCNAC. . ) (POT
547 Missing (in isoform 2).
7FIGLEVSP 00779.
945 C->s: LOSS OF ACTIVITY.
247 S -> G (IN REF. 2 AND 3).
248 S -> M (IN REF. 2).
323 G -> N (IN REF. 2).
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Sequence=VSP_007779;
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Best Local Similarity 100.
Matches 10; Conservative
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323 32
325 32
1015 AA;
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PIR; JC5263; JC5263.
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Genew; HGNC:9677; F
MIM; 601698; -.
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SEQUENCE
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458
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 60.0 , Gapext 60.0
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4: sp_human:*
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6: sp_mammal:*
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8: sp_organelle:*
9: sp_phage:*
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11: sp_rodent:*
11: sp_rodent:*
12: sp_urcebrate:*
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17: sp_archeap:*
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Maximum DB seq length: 200000000
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Perfect score:

Run on:

Sequence:

Scoring table:

Word size :

Searched:

Database :

082656 arabidopsis 083745 rattus norv 064642 rattus norv 090452 rattus norv 090455 brachydanio 064696 mus musculu 091871 xenopus lae 072xn2 xenopus lae 070xn2 xenopus lae 080vn4 homo sapien 090416 homo sapien 075876 homo sapien 091919 xenopus lae 094012 mus musculu 091911 xenopus lae 064605 rattus sp. 091911 xenopus lae 064604 fr. protein-t 064409 mus musculu 044328 musculu 09191 xenopus lae 09401 fr. protein-t 064609 mus musculu 044328 hirudo medi

### ALIGNMENTS

5: sp_invertebrate:*  6: sp_mammal:*  7: sp_mto:*  8: sp_mammal:*  8: sp_mammal:*  10: sp_plant:*  11: sp_virus:*  11: sp_virus:*  12: sp_virus:*  13: sp_virus:*  14: sp_archeap:*  15: sp_archeap:*  17: sp_archeap:*  17: sp_archeap:*  17: sp_archeap:*  18: sp_archeap:*  19: sp_archeap:*  10: sp_batteriap:*  10: sp_batteriap:*  11: sp_archeap:*  12: sp_archeap:*  13: sp_archeap:*  14: sp_archeap:*  15: sp_archeap:*  16: sp_batteriap:*  17: sp_archeap:*  17: sp_archeap:*  17: sp_archeap:*  10: sp_archeap:*  10: sp_archeap:*  11: sp_archeap:*  10: sp_archeap:*  11: sp_archeap:*  12: sp_archeap:*  13: sp_archeap:*  14: sp_archeap:*  15: sp_archeap:*  16: sp_archeap:*  17: sp_archeap:*  18: sp_archeap:*  18: sp_archeap:*  19: sp_archeap:*  10: sp_archeap:*  10: sp_archeap:*  10: sp_archeap:*  11: sp_archeap:*  12: sp_archeap:*  13: sp_archeap:*  14: sp_archeap:*  15: sp_archeap:*  16: sp_archeap:*  17: sp_archeap:*  18: sp_archeap:*  18: sp_archeap:*  19: sp_archeap:*  10: sp_archeap:*  10: sp_archeap:*  10: sp_archeap:*  11: sp_archeap:*  11: sp_archeap:*  12: sp_archeap:*  13: sp_archeap:*  14: sp_archeap:*  15: sp_archeap:*  16: sp_archeap:*  17: sp_archeap:*  18: sp_archeap:*  18: sp_archeap:*  18: sp_archeap:*  18: sp_archeap:*  19: sp_archeap:*  10: s	RESULT 1	Han starting here a	מכ נייי נמאמיישי		Dr. 01-001-2003 (TrEMBLIGI. 25, Last sequence update)	DE PTPN18 protein.		OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	OX NCBI_TaxID=9606;		RC 1155505=Lymph; RX MEDLINE=22388257: PubMed=12477932:		RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,									٠ .		TY and mouse conA sequences.";		RP SEQUENCE FROM N.A.
5: sp_invertebrate:* 6: sp_mammal:* 7: sp_mhammal:* 8: sp_organelle:* 9: sp_phage:* 10: sp_phage:* 11: sp_ordent:* 13: sp_vertebrate:* 14: sp_unclassified:* 15: sp_virus:* 15: sp_rvirus:* 16: sp_pratcheap:* 17: sp_archeap:* 18: sp_organelle:* 17: sp_archeap:* 17: sp_archeap:* 18: sp_archeap:* 19: sp_archeap:* 10: sp_archeap:* 1											chance to have a result being printed.	stribution.				Description		Ostace home sapien	Cocasa nomo sapren	O61152 mus musculu	P70602 rattus norv	Q90y62 brachydanio	Q9nl13 branchiosto	Q93095 homo sapien	Q8n4s3 homo sapien	Q9y1x6 ephydatia f	Ogpouz homo sapien	O7tmp9 mus musculu	Opp664 neurospora	Ognsr5 homo sapien
S S				a: abbud ds : s							No. 1s the number of results predicted by o greater than or equal to the score of the	s derived by analysis of the total score dis	SUMMARIES	<del>sk</del> e	Query	Match Length DB		47.4 301 4	7.0 45.3 1	7.0 453 11	6.3 453 11	258 13	487 5	84 4	292 4	471 5	799 4	802 II	1104 3 0	248 4 0

Result

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100 AYIATQGPLPHTLLDFWRLVWEFGVKVILMAC 131
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tive 0; Mismatches
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01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
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Best Local Similarity 100.1
Matches 32; Conservative
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                                                                                                                                                                                       199 GVPSSPDHMLAMVEBARRLQGSGPBPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDF 258
                                                                                                                                                                                                                  151
                                                                                                                                                                                                                                                259 SLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPHYQNIKENCAPLYDDAL 318
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                                                                                                                                               32 KRCERYWAQEQEPLQTGLFCITLIKEKWINBDIMLRTLKVTFQKESRSVYQLQYMSWPDR
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                                                                                                                              139 KRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDR
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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A STAURDESTER, and Lymphoma;

A STAURDESTER, and Lymphoma;

Strauberg R.;

Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

R EMBL; BC044280; AAH41852.1; --

R EMBL; BC044280; AAH41852.1; --

R GO; GO:0004472; F:protein tyrosine phosphatase activity; IEA.

GO; GO:0004470; F:protein tyrosine phosphatase activity; IEA.

R GO; GO:0006470; F:receptor activity; IEA.

R GO; GO:0006470; F:receptor activity; IEA.

R GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.

InterPro; IPR000342; TyR_PP.

R InterPro; IPR000342; TyR_PP.

R PRINTS; PR00102; Y_Phosphatase.

R PRINTS; PR00109; PTPC; 1.

R PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.

R PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  %1.707-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
8imilar to protein tyrosine phosphatase, non-receptor type 18
(Brain-derived) (Fragment).
                                                                     Length 351;
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                                                                   47.4%; Score 217; DB 4; Length 35
100.0%; Pred. No. 5.2e-213;
ive 0; Mismatches 0; Indels
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Strausberg R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO52800; AAH55800.1; -.
SEQUENCE 351 AA; 38317 MW; SFE9B48C5D0667C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 AA; 40708 MW; 417CA80AA054CF8B CRC64;
                                                                                                                                                                                                                                                                                                                         212 FLRTPQALLAIPRPPGGVLRSISVPGSPGHAMADTYA 248
                                                                                                                                                                                                                                                                                                         319 FLRIPOALLAIPRPPGGVLRSISVPGSPGHAMADIYA 355
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100.0%; Pred. No. 5.4e-213;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                           372 AA.
                                                                  Query Match 47.4% Best Local Similarity 100.0 Matches 217; Conservative
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Best Local Similarity 100.0
Matches 217; Conservative
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SEQUENCE 372 AA;
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259 SLFDVVLKMRKORPAAVQTEEQYRFLYHTVAQMFCSTLQNASPHYQNIKENCAPLYDDAL 318
                                      173 SLFDVVLKWRKQRPAAVQTEEGYRFLYHTVAQMFCSTLQNASPHYQNIKENCAPLYDDAL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . .; IDA.
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061152, 062404;
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Protein-tyrosine phosphatase 18 (EC 3.1.3.48) (PTP-KI) (Fetal liver phosphatase 1) (FLP1) (PTP 49) (PTP HSCF).
PTPN18 OR PTPK1.
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TAXID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; BC008513.; AAH08512.1; -.
GO, MGI:108410; Ptpn18.
GO, GO:0005737; C:cytoplasm; IDA.
GO, GO:0005634; C:nucleus; IDA.
GO, GO:000466; F:non-membrane spanning protein tyrosine phos.
InterPro; IPR000342; TYR_PP.
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01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to protein tyrosine phosphatase, non-receptor type 18.
PTPN18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 453;
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MEDIINE=96329547; PubMed=8695832;
Cheng J., Dalmaru L., Fennie C., Lasky L.A.;
"A novel protein tyrosine phosphatase expressed in
1nn(1o)CD34(hi)Sca(hi) hematopoietic progenitor cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROBLEM: PF001012; Y PhOSPHATASE; 1.
PRINTS; PR00700; PRTYPHFHTASE.
SWART; SW00194; PTPC; TYR
PROSTITE; PS500383; TYR PHOSPHATASE 1; 1.
PROSTITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSTITE; PS50055; TYR_PHOSPHATASE_TP; 1.
Hydrolase; Receptor.
Hydrolase; Receptor.
Hydrolase; Receptor.
Hydrolase; Receptor.
Hydrolase; Receptor.
Hydrolase; Receptor.
                                                                                                                                                                                      233 FLRIPQALLAIPRPPGGVLRSISVPGSPGHAMADIYA 269
                                                                                                                                                   319 FLRTPOALLAIPRPPGGVLRSISVPGSPGHAMADTYA 355
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100.0%; Pred. No. 1.3e-23;
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PTP20 is a positive regulator

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0016787; F:hydrolase activity, IEA.
GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
GO; GO:0004725; F:protein amino acid dephosphorylation; IEA.
InterPro; IPR001247; Protein amino acid dephosphorylation; IEA.
InterPro; IPR001247; TYR PP.
FFIAM: PF00102; Y_phosphatase.
SWART; SM01094; PRTYPHPHTASE.
SWART; SM01094; PTPC; 1.
PROSITE; PS500383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acki, N, Yamaguchi-Aoki, Y, Ullrich A.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U69673; AAC52896.1; -.
HSSP; Q06124; 28HP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             453 AA; 50106 MW; 6CCC132206FB69AE CRC64;
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
Protein tyrosine phosphatase 20.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=97067206; PubMed=8910608;
Acki N., Yamaguchi-Acki Y., Ullrich A.;
The novel protein-tyrosine phosphatase P
of Polz cell neuronal differentiation.",
J. Biol. Chem. 271:29422-29426(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.3:
Best Local Similarity 100.
Matches 29; Conservative
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                                                                                                                                                  Mammalia; Eutheria
NCBI_TaxID=10116;
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SEQUENCE
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Q90Y62
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RHSSP, Q06124; ZSHP.

RHSSP, Q06124; ZSHP.

RHSSP, Q06124; ZSHP.

RG; G0:0005634; C:nucleus; IDA.

RG; G0:0004726; F:non-membrane spanning protein tyrosine phos. . .; IDA.

RG; G0:0004726; F:non-membrane spanning protein tyrosine phos. . .; IDA.

RG; G0:000422; TYR_phosphatase.

RITHERPRO; IPRO0032; TYR_phosphatase.

REART; SMO0194; PTPC; ITR_PROSPHATASE.

RNGART; SMO0194; PTPC; ITR_PROSPHATASE.

RROSITE; PS50055; TYR_PHOSPHATASE.

RW Hydrolase; Nuclear profein; Alternative splicing.

RW Hydrolase; Nuclear profein; Alternative splicing.

RW Hydrolase; Nuclear profein; Alternative splicing.

FT DOMAIN

FT ACT SITE 229 BY SIMILARITY.

FT CONPLICT 11 11 F - - L (IN REF. 3).

"TRICKEN; TYREP. 36201 MW; 89ADTE73CE8136B0 CRC64;
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
STRAIN=C57BL/6; TISSUE=FETAL LIVER;
MEDLINE=97131769; PubMed=9977243;
MEDLINE=97131769; PubMed=9977243;
T. Cloning and characterization of fetal liver phosphatase 1, a nuclear protein tyrosine phosphatase isolated from hematopoietic stem cells.";
Ellood 88:4510-4525(1996).
C. -- FUNCTION: MAY BE INVOLVED IN GROWTH AND DIFFERENTIATION OF HEMATOPOIETIC CELLS.
C. -- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN TYROSINE + PHOSPHATE.
C. -- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
C. -- ALTERNATIVE PRODUCTS:
C. SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
C. -- ALTERNATIVE PRODUCTS:
C. SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
C. SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
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                                                                                                                                  Huang K., Sommers C.L., Grinberg A., Kozak C.A., Love P.E., "Cloning and characterization of PTP-K1, a novel nonreceptor protein tyrosine phosphatase highly expressed in bone marrow."; Oncogene 13:1567-1573 (1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISOId-O61152-2; Sequence=VSP_050405;
-!-TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BONE MARROW. ALSO
EXPRESSED IN KIDNEY. LUNG, OVARY, SPLEEN, THYMUS AND LYNGH NODE.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN THE EMBRYO FROM DAY 15.5.
-!- SIMILARITY: BELCONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY.
EMBL; U35124; AAB82736.1; -.
EMBL; U49835, AAB18623.1; -.
EMBL; U52523; AAG52991.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q61152-1; Sequence=Displayed;
                                                                                                                MEDLINE=97030045; PubMed=8875997;
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      Blood 88:1156-1167(1996)
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Best Local Similarity
Matches 32; Conserv
                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=FLP1B;
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P70602
ID P7060
AC P7060
DT 01-FF
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SOLUTION SUND SERVICE

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MEDLINE=21076097; PubMed=11206415;
MEDLINE=21076097; PubMed=11206415;
MEDLINE=21076097; PubMed=11206415;
MEDLINE=21076097; PubMed=11206415;
MEDLINE=21076097; PubMed=11206415;
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MEDLINE=21076097; PubMed=11206415;
MEDLINE=21076097; PipMed=2107697; PipMed=2107697;
MEDLINE=2107697; PipMed=2107697; Pip
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DTA-2003 (TrEMBLrel. 24, Last annotation update)
Receptor PTP-like protein IA-2 (Fragment).
Brachydanio rezio (Zebrafish) (Danio rezio).
Brachydanio rezio (Zebrafish) (Caniata; Vertebrata; Euteleostomi;
Brachydanio Neopterygii; Teleostei; Ostatiophysi; Cypriniformes;
Cyprinidae; Danio.
NCBL TaxID-7955;
                                                                                          Gaps
                                                                                  ;
        Length 453;
6.3%; Score 29; DB 11; Length 45
100.0%; Pred. No. 1.5e-20;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 AA
                                                                                                                                                                    430 GAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
                                                                                                                                                                                                                                     425 GAOTGGLGFNLRIGRPKGPRDPPAEWTRV 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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453 AA.

P70602 PRELIMINARY; PRT; P70602; 01-FEB-1997 (TrEMBLrel. 02, Created)

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2.4%; Score 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 HCSAGCGRTGV 77
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase.
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SEQUENCE
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Ono-Koyanagi K., Suga H., Katch K., Miyata T.;
"Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
divergence of tissue-specific isoform genes in the early evolution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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093095,
091FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-FEB-1997 (TrEMBLrel. 24, Last annotation update)
Protein tyrosine phosphatase PEP (EC 3.1.3.48) (Fragment).
Protein tyrosine phosphatase PEP (EC 3.1.3.48) (Fragment).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Branchiostoma belcheri (Amphoxius).
Eukaryota, Metazoa, Chordata, Cephalochordata, Branchiostomidae,
Branchiostoma.
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EMBL; AB033564; BAA95171.1; -.

HSSP, P18052; 1YFO.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.

GO; GO:0004735; F:protein amino acid dephosphorylation; IEA.

InterPro; IPR000242; TYR_phosphatase.
                                                                                                                             Query Match 2.6%; Score 12; DB 13; Length 258; Best Local Similarity 100.0%; Pred. No. 0.0023; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.6%; Score 12; DB 5; Length 487;
ilarity 100.0%; Pred. No. 0.0041;
Conservative 0; Mismatches 0; Indels
                                                                  NON TER 1 1
SEQUENCE 258 AA; 29544 MW; 93FBC53CAA4EA4A2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
AMPTPR4c protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                 487 AA.
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PRINTS; PR00700; PRTYPHPHTASE.
SMART; SM00194; PTPC; 2.
PROSITE; PS00313; TYR_PHOSPHATASE_1; 2.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_2FP; 2.
PROSITE; PSS0056; TYR_PHOSPHATASE_2; 1.
PROSITE; PSS0055; TYR_PHOSPHATASE_PTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 AYIATQGPLPHT 278
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ses 12; Conserv
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                                          Hydrolase.
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SEQUENCE
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Matches
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SEQUENCE FROM N.A.

A DAYLON M.A., Knobloch T.J.;

Bayton M.A., Knobloch T.J.;

Bayton M.A., Knobloch T.J.;

Bayton M.A., Knobloch T.J.;

Ind fibroblast cell line WI-38.";

Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.

REMEL; U69700; AAB09079.1; -.

RASP; P29350; 1GWZ.

GO; GO:0004727; F:prenylated protein tyrosine phosphatase act. .; IEA.

GO; GO:0004727; F:prenylated protein tyrosine phosphatase act. .; IEA.

GO; GO:0004727; F:prenylated protein tyrosine phosphatase act. .; IEA.

GO; GO:000472; F:prenylated protein tyrosine phosphatase act. .; IEA.

GO; GO:000427; F:prenylated protein tyrosine phosphatase act. .; IEA.

DR FRONTER: PRO0102; Y: Phosphatase; 1.

PRINTS; PRO0700; PRTYPHPHTASE.

PRINTS; PRO0700; PRTYPHPHTASE.

PROSITE; PSO0383; TYR_PHOSPHATASE.1; 1.

PROSITE; PSO055; TYR_PHOSPHATASE.2; 1.

PROSITE; PSO055; TYR_PHOSPHATASE.2; 1.
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01-OCT_2002 (TrEMBLrel. 22, Last sequence update)
01-OCT_2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Hypothetical protein (Fragment).
Eukan septems (Human).
Hypothetical protein (Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberger, Submitted (JUL-2012) to the EMBL/GenBank/DDBJ databases.

Submitted (JUL-2012) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0005483 F: Sinding; IEA.

R GO; GO:0005488 F: Sinding; IEA.

R GO; GO:0006402 F: Protein tyrosine phosphatase activity; IEA.

GO; GO:0006402 F: Protein amino acid dephosphorylation; IEA.

GO; GO:0006410; P: Protein amino acid dephosphorylation; IEA.

R GO; GO:0006810; P: Protein amino acid dephosphorylation; IEA.

R GO; GO:0006810; P: Protein amino acid dephosphorylation; IEA.

R InterPro; IPR001993; Mitch Garrier.

R InterPro; IPR001993; PTPC_mCif.

R InterPro; IPR0000387; TYR_PP.

R Pfam; PF00102; Y_Dhosphatase; 1.

R PRINTS; PR00100; PRTYPHPHTASE.

R SMRRT; SM00194; PTPC_mCif; 1.
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0
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100.0%; Pred. No. 0.0089;
ative 0; Mismatches 0; Indels
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84 84
84 AA, 9699 MW; 4DA40B7BA38E45DA CRC64;
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PROSITE; PS00215; MITOCH CARRIER; 1.
PROSITE; PS50083; TYR_PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE 2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
HYPOTHELICAL protein.
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TISSUE=Renal adenocarcinoma;
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DB 4;

Length 799;

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REMBL; AF150732; AAF67472.1; -...
R RSSP; P29350; 1GWZ.
R GO, GO:0016787; F:hydrolase activity; IEA.
GO, GO:000470; P:protein tyrosine phosphatase activity; IEA.
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
R InterPro; IPR000242; TYr PP.
R PIGHTS; PR00700; PRTYPHPHTASE.
R PRINTS; PR00700; PRTYPHPHTASE.
R PRINTS; SM00194; PTPc; 1.
R PROSITE; PS0056; TYR_PHOSPHATASE_1; 1.
R PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.
R PROSITE; PS0055; TYR_PHOSPHATASE_2; 1.
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                          799 AA; 90610 MW; 93F5385016F33D0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
2.4%; Score 11; DB 4;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 11; Conservative 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              228 HCSAGCGRTGV 238
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                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase.
SEQUENCE
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                                   Gaps
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Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Huang C., Zhang C., Wu T., Peng Y., Gu Y., Zhang L., Jiang C.,
Han Z., Wang Y., Chen Z., Fu G.;
"A novel gene expressed in human adrenal gland.";
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Eukaryota, Metazoa, Porifera, Demospongiae, Ceractinomorpha,
Haplosclerida, Spongillidae, Ephydatia.
NCBI_TaxID=31330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 2.4%; Score 11; DB 5; Length 471; Local Similarity 100.0%; Pred. No. 0.042; nes 11; Conservative 0; Mismatches 0; Indels
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        471 AA; 54509 MW; 7DA62456154A6A56 CRC64;
                                                                                                                                                                                                                                                                                                      Q91IX6;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
SPTPR4 (Fragment).
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Protein tyrosine phosphatase.
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100.0%; Pred. No. 0.027; tive 0; Mismatches (
                                                                                                                                                                                                                                                                                    471 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWART; SM00194; PTPC; 2.
PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
PROSITE; PS50056; TYR_PHOSPHATASE 2; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
                                                                                                                                                                                                                                                                                 PRT;
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                                11; Conservative
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                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                      59 KNRYKDVLPYD 69
                                                                                                                             52 KNRYKDVLPYD 62
  Best Local Similarity
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AC 099001
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=CSTRAIN-GENERAL TISSUE=Hematopoietic Stem Cell;

MIDLINE=22388257; PubMed=12477932;

RA Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.P., Zeeberg B. Buetow K.H., Schemen C.M., Schuler G.D.,

RA Altschul S.P., Zeeberg B. Buetow K.H., Schemen C.M., Schuler G.D.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

RA Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

ROSAK S.A., McKernan P.J., McKernan R.J., Malke J.A., Gunarane P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley W.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marza M.A.,

RA Mones S.J., Marza M.A.,

RA Marza M.A., Rading M. I.S., Robit L. I.L., Rading D. M.C.,

RA Marza M.A., Rading M. I.S., Rading D. M.C.,

RA Marza M.A., Rading M. I.S., Rading D. I.L., Rading D. I.L., Rading D. I.L
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Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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0; Indels
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Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC055377; AAH55377.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB8C3AA618B28561 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QTTMP9 PRELIMINARY; PRT; 802 AA. Q7TMP9; 0.1-OCT-2003 (TrEMBLrel. 25, Created) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein tyrosine phosphatase, non-receptor type 8.
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100.0%; Pred. No.
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Best Local Similarity
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Sordariomycetidae; Sordariales; Sordariaceae; Neurospora
                                                                                                                                                                        SEQUENCE FROM N.A
                      NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20068798; PubMed=10600535; Apoyana K., Matsuda T., Aoki N.; Macyana K., Matsuda T., Aoki N.; Characterization of newly identified four isoforms for a putative cytosolic protein tyrosine phosphatase PTP36."; Biochem. Blophys. Res. Commun. 266:523-531(1999).
EMBL; AF170903; AAF27549.1; -. HSSP; Q06124; 28HP.
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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R MGD; MGI:102467; Ptpn14.

R GO; GO:0016787; P:hydrolase activity; IEA.

GO; GO:0016787; P:hydrolase activity; IEA.

GO; GO:000470; P:hydrolase activity; IEA.

R GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.

InterPro: IPR000389; Band 4.1.

R InterPro: IPR000389; TYR Phosphatase.

R PEAM; PF00373; Band 4.1.

R PRINTS; PR0035; BAN41.

R PRINTS; PR0035; BAN41.

R RANTS; PR00195; BAN41.

R RANT; SM00194; PTPC; 1.

R RANT; SM00194; PTPC; 1.

R PROSITE; PS00661; FERM 2; 1.
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Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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.00.0%; Pred. No. 0.071;
    Indels
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
PTP36-B isoform.
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Last annotation update)
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    Mismatches
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I-ORT-2001 (TrEMBLrel. 16, Last sequenc
01-OCT-2003 (TrEMBLrel. 25, Last annotat
Related to protein-tyrosine-phosphatase.
                                                                                                                                                                                                 PRT;
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1es 11; Conservative
    11; Conservative
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                                             228 HCSAGCGRTGV 238
                                                                                      226 HCSAGCGRIGV 236
                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=DDY
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Q9P664;
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Matches
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                                                                                                                                                          RESULT 13
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Gaps
                                        Fartmann B., Holland R.,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                      R RSSP; PS2350; 1GWZ.

R GO; GO: 0005488; F: binding; IEA.
GO; GO: 00016787; F: bydrolase activity; IEA.
GO; GO: 00016787; F: bydrolase activity; IEA.
GO; GO: 00016787; F: bydrolase activity; IEA.
GO; GO: 0006470; F: protein tyrosine phosphatase activity; IEA.
GO; GO: 0006410; P: protein tyrosine phosphatase activity; IEA.
GO; GO: 0006810; P: transport; IEA.
R InterPor; IPR001993; Mitoch_carrier.
R InterPor; IPR001993; Mitoch_carrier.
R InterPor; IPR001993; Mitoch_carrier.
R InterPor; IPR001942; TYR_phosphatase.
R PRINTS; PR001024; TyR_phosphatase.
R PRINTS; PR00102; Y_phosphatase.
R PRINTS; PR00106; RHOP; I.
R PROSITE; PS00215; MITOCH_CARRIER; I.
R PROSITE; PS00215; MITOCH_CARRIER; I.
R PROSITE; PS00215; MITOCH_CARRIER; I.
R PROSITE; PS00215; TYR_PHOSPHATASE_2; I.
R PROSITE; PS00265; TYR_PHOSPHATASE_2; I.
R PROSITE; PS50056; TYR_PHOSPHATASE_2; I.
R PROSITE; PS00056; TYR_PHOSPHATASE_PTP; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Amygdala;

A Ansorge W. Witner U., Mewes H.W., Weil B., Wiemann S.;

A Ansorge W. Witner U., Mewes H.W., Weil B., Wiemann S.;

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

R EMBL; ALI57451; CAB75665.1; -.

R PIR; T46903; TG4903.

R GO; GO:0006709; F:hydrolase activity; IEA.

R GO; GO:0006470; F:hydrolase activity; IEA.

R GO; GO:0006470; F:protein thing acid dephosphorylation; IEA.

R InterPro; IPR000387; TYR, Phosphatase.

R InterPro; IPR000242; TYR, Phosphatase.

R InterPro; PR00102; Yyr, PP.

R PEMR: FF00102; Yyr, PP.

R PRIMTS; PR00100; PRTYPHTASE.

R PRIMTS; SM00194; PTPC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1104 AA; 120371 MW; 5D25498BCFF7FF22 CRC64;
SEQUENCE FROM N.A. Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B. Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                             German Neurospora genome project;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL AL355938, CAB91306.2;
HSSP; P29350; 1GWZ.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein (Fragment).
DKFZPP61A0712.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.4%; Score 11; DB Local Similarity 100.0%; Pred. No. 0.0 ies 11; Conservative 0; Mismatches
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DR PROSITE; PS00363; TYR\_PHOSPHATASE\_1; 1.

DR PROSITE; PS50056; TYR\_PHOSPHATASE\_2; 1.

DR PROSITE; PS50056; TYR\_PHOSPHATASE\_PTP; 1.

XW HYPOTHERICAL PIOTEIN; HYDROLASE.

FT NON TER 1

QUETY MAICH 248 AA; 28304 MW; EE10C57FBC5B5114 CRC64;

QUETY MAICH 2.2%; Score 10; DB 4; Length 248;

Best Local Similarity 100.0%; Pred. No. 0.25;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps

QY 100 ANIATQGPLP 109

DD 48 ANIATQGPLP 57

0

Search completed: August 17, 2004, 20:52:34 Job time : 49 secs

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# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

August 17, 2004, 20:41:49; Search time 19 Seconds (without alignments) 1244.459 Million cell updates/sec US-10-087-993A-36 2424 1 MSRSLDSARSFLERLEARGG.......NLRIGRPKGPRDPPAEWTRV 458 Title: Perfect score: Sequence: Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

389414 seqs, 51625971 residues Searched:

389414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgg2\_6/ptcdata/2/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptcdata/2/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptcdata/2/iaa/6A\_COMB.pep:\*
5: /cgn2\_6/ptcdata/2/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptcdata/2/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptcdata/2/iaa/PCTUS\_COMB.pep:\* Issued Patents AA:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	Sequence 2, Applia Sequence 7, Applia Sequence 17, Applia Sequence 18, Applia Sequence 18, Applia Sequence 19, Applia Sequence 20, Applia Sequence 16, Applia Sequence 16, Applia Sequence 16, Applia Sequence 2, Applia Sequence 117, Applia Sequence 117, Applia Sequence 119, Applia Sequence 5, Applia	equence 5, equence 13, equence 13, equence 12,
4	0.8 - 821 . 2.7 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	US-09-282-257-5 US-08-685-992-13 US-09-144-925-13 US-08-685-992-12 US-09-144-925-12
DB		
Length		$\sigma \omega \omega \omega \omega$
تبنة	6.00 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	
Score	H	വവവവ
Result No.	 	2000 4000 7000

38,	equence 21, equence 2, equence 2, equence 2,	- 40-	Sequence 19, Appl Sequence 19, Appl Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli
08-202-389 08-446-345 09-848-294	-00-100-200-200-200-200-200-200-200-200-		-09-685-992- -09-685-992- -08-036-292- -08-449-609-
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593 232 913	242 242 1337 1337 1337	4477 447 447 460 487	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
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TH 00 TH F	44 44 41 435 435 535 535	4 2 4 3 3 4 4 2 6 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	4 4 4 4 0 4 4 4 4 0 4 4 4 4 0 5 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
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## ALIGNMENTS

	2;	09	120	120	180	180	240	240	300	300	360	360	419	414
RESULT 1 US-08-821-278A-2 Sequence 2, Application US/08821278A Sequence 2, Application US/08821278A Fatent No. 6238902 GENERAL INFORMATION: APPLICANT: Cheng, Jill APPLICANT: Cheng, Jill APPLICANT: Protein Tyrosine Phosphatases FILE REFERENCE: P10.0R FULE REFERENCE: P10.0R CURRENT APLICATION NUMBER: US/08/821,278A CURRENT FILING DATE: 1997-03-20 NUMBER OF SEQ ID NOS: 23 SEQ ID NO 2 LENGTH: 453 TYPE: PRT TYPE: PRT CORGANISM: Mus Musculus US-08-821-278A-2	Query Match 73.4%; Score 1778.5; DB 3; Length 453; Best Local Similarity 74.9%; Pred. No. 7.9e-154; Matches 344; Conservative 32; Mismatches 76; Indels 7; Gaps	OY 1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN 6	61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW	61 RYKDVVAYDETRVILSLLQEEGHGNYINANFIRGIDGSQAYIATQGFLPHTLLDFWRLVW	DERYMAQEQEPLOTGLECITLIKEKWLNEDIMLRTLKVTF	Db 121 BFGVKVILMACQBTBNGRRKCERYWARBQBPLKAGPFCITLIKETTLNADITLRTLQVTF 1	OY 181 QXESRSVYQLQYMSWPDRGVPSSPDHMLAMVEBARLQGSGFBPLCVHCSAGGGRTGVLC 2.	Db 181 QKEFRSVHQLQYMSWPDHGVPSSSDHILTMVBEARCLQGLGFGFLCVHCSAGGGRTGVLC 2	Qy 241 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 3	Db 241 AVDYVRQLILITQTIPPNFSLFQVVLEMRKQRPAAVQTEEQYRFLYHTVAQLFSRTLQDTS 3	Qy 301 PHYQNIKENCAPLYDDALFLETFQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKR 3	DD 301 PHYQNLKENCAPICKEAFSLRTSSALPATSRPPGGVLRSISVPAPPTLPMADTYAVVQKR 3	OY 361 GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLP-GRVPADQSPA 4	Db 361 GASAGIGPGPRAPTSTDIPIXSQVAPRAQRPVAHTEDAQGTTALRRVPADQNSS 4.

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181 QKESRPVHQLQYMSWPDHGVPSSSDHILTMVEEARCLQGLGPGPLCVHCSAGCGRTGVLC 240
                                                                                                                                                                                                                   301 PHYONIKENCAPLYDDALFLRIPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKR 360
                                                                                                                                                                                                                                                                                                                                                                                                           241 AVDYVRQLLLTQTIPPNFSLFEVVLEMRKQRPAAVQTEEQYRFLYHTVAQLFSRTLQNNS
                                                                                                                                                                                                                                                                                                                                                             361 GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLP-GRVPADQSPA
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TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHAIASE PTP20
AND RELATED PRODUCTS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               420 GSGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
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APPLICATION NUMBER: US/09/430,626A
FILING DATE: 29-0ct-1999
CLASSIFICATION: «Unknown-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/951,260
FILING DATE: October 16, 1997
APPLICATION NUMBER: 06/030,660
FILING DATE: No. 6482605ember 13, 1996
APPLICATION NUMBER: POT/1897/00946
FILING DATE: Unme 17, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0
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REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 227/004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 453 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPHOGOY: linear
MOLECTUE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-430-6268-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09430626A Patent No. 6482605 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Aoki, Nachito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-430-626A-7
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                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Acki, Nachito
APPLICANT: Ulizich, Ack
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       420 GSGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
                                                     CILL.
STATE: CALLLCL.
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
CURRENT APPLICATION NOTES:
TILING DATE: October 16, 1997
TILING DATE: October 16, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/030,860
FILING DATE: No. 6004791ember 13, 199
APPLICATION NUMBER: PCT/1897/00946
FILING DATE: June 17, 1997
ATTORNEY/AGENT INFORMATION:
NAWE: Warburg, Richard J.
REGISTATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 227/004
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                     Sequence 7, Application US/08951260A Patent No. 6004791 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (213) 489-1600
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TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: peptide
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COMPUTER REALBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 8.5 Extorage
COMPUTER: 1BM Compatible
OPERATING SYSTEM: 1BM P.C. DOS 5.0
SOFWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/081,345
FILING DATE: Herewith
Sequence 18, Application US/09081345
Patent No. 622641
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047,222
FILING DATE: May 20, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 234/253
TELEFRONGINICATION INFORMATION:
TELEFRONG: (213) 955-0440
TELEFAX: (213) 955-0440
INFORMATION FOR SO ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 802 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 161; Conserva
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                                                                                                                                                                                                                                                                                                                                                                    QKESRPVHQLQYMSWPDHGVPSSSDHILTMVEEARCLQGLGPGPLCVHCSAGCGRTGVLC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120
                                                                                                                                                                                                                                                                                                                                     EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                        QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEBARRLQGSGPEPLCVHCSAGCGRTGVLC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVDYVRQLLLTQMIPPDFSLFDVVLKWRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 PHYONIKENCAPLYDDALFLRTPOALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEOKR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLP-GRVPADQSPA 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 LLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIEN 136
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                                                                                                                                  1 MSRQSDLVRSFLEQQEARDHRKGAILAREFSDIKARSVAWKTEGVCSTKAGSQQGNSKKN
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                                                                                                1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN
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                                           7; Gaps
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         Best Local Similarity 74.5%; Pred. No. 1.2e-151;
Matches 342; Conservative 37; Mismatches 73; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Cheng, Jill
APPLICANT: Lasky, Laurence A.
TILLE OF INVENTION: Protein Tyrosine Phosphatases
FILE REFERENCE: P1010R1
CURRENT APPLICATION NUMBER: US/08/821,278A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ. ID NOS: 23
SEQ. ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
34.2%; Score 830; DB 3; I
Best Local Similarity 100.0%; Pred. No. 5.5e-68;
Matches 155; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-821-278A-17; Sequence 17, Application US/08821278A; Patent No. 6238902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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RESULT 5 US-09-081-345-18

147 QEQE-PLOTGLFCITLIKEKWINEDIMIRTLKVTFQKESRSVYQLOYMSWPDRGVPSSPD 205 203 206 HMLAMVEEARRLOGSGPEPLCVHCSAGCGRIGVLCTVDYVRQLLLITQMIPPDFSLFDVVL 265 204 PILQLIWDMRCYQEDDCVPICIHCSAGGGRIGVICAVDYTWMLLKDGIIPKNFSVFNLIQ 263 KYRKORPAAVOTEEQYRFLYHTVAQMFCSTLQNASPHYQNIKENCAPLYDDALFLRTPQA 325 LLAIPRPPGGVLRSISVPGS-----PGHAMAD--TYAEEQKRGAPAGAGSGTQTGTGT 377 84 25 ASEFLKIKROSTKYKADKIYPTTVAQRPKNIKKNRYKDILPYDHSIJVELSLITSDEDSSY 87 INGNFIRGUDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA 27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY 31; DB 3; Length 802; 31.2%; Score 755.5; DB 3; Length ilarity 44.0%; Pred. No. 3.6e-60; Conservative 55; Mismatches 119; Indels ΟF TREATMENT DISORDERS 309 8 ద

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147 QEQE-PLOTGLECITLIKEKWINEDIMLRTLKVTPOKESRSVYQLOYMSWPDRGVPSSPD 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 INASPIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYRILVIVMACMEFEMGKKKGERYWA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 HMLAMVEBARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ASEFLKIKRQSTKYKADKIYPTTVAQRPKNIKKANYKDILPYDHSLVELSLLTSDEDSSY
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                        266 KMRKORPAAVOTEEOYRFLYHTVAOMF---CSTLONASPHYONIKENCAP 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266 KMRKORPAAVOTEEQYRFLYHTVAQMFCSTLONASPHYONIKEN 309
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                                                                                                             US-00-12, 278A-18
Sequence 18, Application US/08821278A
Sequence 18, Application US/08821278A
Sequence 18, Application US/08821278A
Sequence 18, Application US/08821278A
SEPLICANT: Lasky, Laurence A,
TILLE OF INVENTION: Protein Tyrosine Phosphatases
FILE REFERENCE: P1010R1
CURRENT APPLICATION NUMBER: US/08/821,278A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1.4. Application US/08821278A

Sequence 1. Application US/08821278A

GENERAL INFORMATION:
GENERAL INFORMATION:
THILE OF INVENTION:
FILLE REFERENCE:
CURRENT APPLICATION NUMBER: US/08/821,278A

CURRENT FILING DATE: 1997-03-20

NUMBER OF SEQ ID NOS: 23

SEQ ID NO 12

LENGTH: 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
29.5%; Score 715.5; DB 3;
Best Local Similarity 48.9%; Pred. No. 3.5e-57;
Matches 139; Conservative 45; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 47.1%
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo Sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 QEQE-PLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 HMLAMVEBARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
30.0%; Score 727.5; DB 3;
Best Local Similarity 46.9%; Pred. No. 1.3e-57;
Matches 136; Conservative 56; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FRSESEQ for Windows 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081,345 FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 234/253
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-040
TELEFAX: (213) 955-040
ITELEFAX: (213) 955-040
STELEY: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                              Sequence 2, Application US/09081345
Patent No. 6228641
GENERAL INFORMATION:
APPLICANT: Bahija Jallal
APPLICANT: Gregory D. Plowman
TITLE OF INVENTION: PIPO4 RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/047,222
FILING DATE: MAY 20, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                        NUMBER OF SECUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEB: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               807 amino acids
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MOLECULE TYPE: peptide
US-09-081-345-2
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STATE: California
COUNTRY: U.S.A.
                                              363 TMNAEE 368
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      378 ARSAEE 383
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                                                                                                             RESULT 6
US-09-081-345-2
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167 INEDIMLRT----LKVTFQKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGP 222
                                                                                                                                                                              233 EPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVLKWRKQRPAAVQTEEQYR 282
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                                                                                                                 64 LANTVIDFWRMVWEYNVVIIVMACREFEMGRKKCERYWPLYGEDPITFAPFKISC----
    108 LPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYW-AQEQEPLQTGLFCTTLIKEKW
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; Sequence 20, Application US/09144925
; Ratent No. 5951979
; GENERAL INFORMATION:
; APPLICANT: TONKS, Nicholas
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; CORRESPONDENCE ADDRESS:
3 CORRESPONDENCE ADDRESS:
5 CORRESPONDENCE HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
CORRESPONDENCE MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.4%; Score 665; DB 2;
49.4%; Pred. No. 1.2e-52;
tive 44; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastENG for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSHL96-03Z
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CLASTPECATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,99
FILING DATE: J119 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20:
                                                                                                                                                                                                                                                                      283 FLYHTVAQMECSTLQ 297
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237 LVHRAIAQLFEKQLQ 251
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amino acid
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ZIP: 02421-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 126; Conservative
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Best Local Similarity
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                                                                                                                                                           122 LYGEDPITFAPFKIS-CEDEQARTDYFIRTLILEFQNESRRLYQFHYVNWPDHDVPSSFD 180
                                                                                                                                                                                                                                                62 INANFIKGVYGPKAYVATQGPLANTVIDFWRMVWEYNVVIIVMACREFEMGRKKCERYWP 121
                                                                                                                               146 AQEQEPLQTGLFCITLIKEKWINEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD 205
                                                                                                                                                                                                                      206 HMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 265
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2 ARDFMRLRRLSTKYRTEKIYPTATGEKEENVKKNRYKDILPFDHSRVKLTLKTPSQDSDY
                                          87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYW-
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                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-685-992-20
| Sequence 20, Application US/08685992
| Patent No. 5912138 |
| Patent No. 5912138 |
| GENERAL INFORMATION: APPLICANT: Tonks, Nicholas APPLICANT: Flint, Andrew J. TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN ITILE OF INVENTION: TYROSINE PHOSPHATASES NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESS: ADDRESSE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C. STREET: Two Militia Drive CITY: Learnington STREET: MAINT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,992
FILING DATE: 25-UUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION: A35
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                266 KMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQ 297
                                                                                                                                                                                                                                                                                                                                                      241 EMRTORHSAVOTKEOYELVHRAIAOLFEKOLO 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL
TELECHONICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEPAX: 781-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / MOLECULE TYPE: peptide US-08-685-992-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
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47 STVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQG 106
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                               PEPLCVHCSAGCGRIGVLCTVD-YVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQ 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 LNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARR-----LQGSG 221
167 INEDIMIRTLKVTFOKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEBARR-----LQGSG 221
                                                                                                               3 SQMVASASENNAKNRYRNVLPYDWSRVPLKPIHEEPGSDYINASFMPGLWSPQEFIATQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Gaps
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                                                                                                                                                                                                                                                                                       Ge-09-144-925-16
Sequence 16, Application US/09144925
Sequence 16, Application US/09144925
Patent No. 5951979
GENERAL INFORMATION:
APPLICANT: Tonke, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Leaington
STATE: MA
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,925
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

20.4%; Score 493.5; DB 2
Best Local Similarity 43.6%; Pred. No. 5.5e-37;
Matches 115; Conservative 36; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSHL96-03Z
                                                                                                                                                                                                     235 YVFLH----QCICGS-SNSQPRPQ 253
                                                                                                                                                                          281 YRFLYHTVAQMFCSTLQNASPHYQ 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,992
FILING DATE: UNIV 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 255 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           781-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide US-09-144-925-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 STVAGSRPENVRKONRYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQG 106
      64 LANTVIDFWRMVWEYNVVIIVMACREFEMGRKKCERYWPLYGEDPITFAPFKISC---- 118
                                                                                                                                                            167 INEDIMIRT----IKVTFQKESRSVYQLQYMSWPDRGVPSSPDHMIAMVEEARRLQGSGP
                                                                           223 EPLCVHCSAGCGRIGVLCTVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTBEQYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOMVASASENNAKARYRNVLPYDWSRVPLKPIHEEPGSDYINASFMPGLWSPQEFIATOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 20.4%; Score 493.5; DB 2; Best Local Similarity 43.6%; Pred. No. 5.5e-37; Matches 115; Conservative 36; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, STREEF: Two Militia Drive STREEF: Two Militia Drive STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: PESESEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,992
FILING DATE: 25-UUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/08685992
Patent No. 5912138
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYGSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSHL96-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Petricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL
TELECHONE: 781-861-6240
TELEFHONE: 781-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                       237 LVHRAIAQLFEKQLQ 251
                                                                                                                                                                                                                          283 FLYHTVAQMFCSTLQ 297
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , TOPOLOGY: linear
, MOLECULE TYPE: peptide
US-08-685-992-16
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STRANDEDNESS: sin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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1305 RVKQLQFTTWPDHSVPBAPSSLLAFVBLVQEQVQATQGKG--PILVHCSAGVGRTGT--- 1359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 IMACREIENGRKRCERYWAGEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKES--- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 EGAVLAG---EFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLL
                                                                242 VDYVRQLLLTQMIPPD--FSLFDVVLKMRKQRPAAVQTEEQYRFLY 285
                                                                                                                                                             19.3%; Score 467; DB 1; Length 59: 32.9%; Pred. No. 4.8e-34; ive 57; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/202,389
FILING DATE: 28-FBB-1994
CLASSIPICATION: 435
PRIOR APPLICATION NUMBER: US/08/3,926
FILING DATE: 01-DEC-1992
FILING DATE: 01-DEC-1992
FILING DATE: 01-DEC-1992
FILING DATE: 31-JAN-1992
FILING DATE: 31-JAN-1992
FILING DATE: 32-JAN-1992
FILING DATE: 26-UNN-1992
FILING DATE: 26-UNN-1991
FILING DATE: 26-UNN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Granahan, Patricia
REGISTATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: B1H92-05MA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 595 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 32.9
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-08-202-389-6
                                                                                                                                                                                                                                                                                                                                                                                                                                Lexington
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                                                                                                                                    RESULT 14
US-08-202-389-6
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CITY: Le
STATE: M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 QTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILM 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 ACREIENGRKRCERYWAQEQEPLOTGLFCITLIKE----KWLNEDIMLRTLKVTFQKESR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUYQLQYMSWPDRGVPSSPDHMLAMV----EEARRLQGSGPBPLCVHCSAGGGRTGVLCT 241
123 MENWIVLLLLQVEEQK-TLSVRQFHYQAWPDHGVPSSPDTLLAFWRMLRQWLDQTMEGGP 181
                                                              P---IVHCSAGVGRIGILIALDVILRQLQSEGLLGP----FSFVRKWRESRPLMVQTEAQ 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 SFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYD 69
                                       222 PEPLCYHCSAGCGRTGVLCTVD-YVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQ
                                                                                                                                                                                                                                                                                                        APPLICANT: MAURO, LAURA J.
APPLICANT: MAURO, LAURA J.
APPLICANT: MAURO, LAURA J.
APPLICANT: MAURO, LAURA J.
APPLICANT: DAVIS, ALAN R.
APPLICANT: DIXXON, JACK E.
TITLE OF INVENTION: OSTEOBLAST-TESTICULAR PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,930
FILING DATE: 21-NOV-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICALL...
FILING DATE:
CLASSIPICATION: 435
ATTOCNEY/AGENT INFORMATION:
NAME: KONEXI, ANTOINETTE F.
REGISTATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 20344-20975.00
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 813-6600
TFLEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.6%; Score 474; 39.9%; Pred. No. 5
                                                                                                                                          235 YVFLH----QCICGS-SNSQPRPQ 253
                                                                                                                  281 YRFLYHTVAQMFCSTLQNASPHYQ 304
                                                                                                                                                                                                                                                    Sequence 2, Application US/08342930 Patent No. 5821084 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1711 amino acids
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 39.98
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                          182
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                                                                                                                                             348 VMTTREVEKGRNKCVPYWPEVGMQRAYGPYSVTNVGEHDTTE-YKLRTLQVSPLDNGDLI 406
                                       RSVYQLQYMSWPDRGVPSSPDHMLAMVEBARRLQGSGPE--PLCVHCSAGCGRTGVLCTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGAVLAG---EFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLL
                                                                243 DYVROLLLTQMIPPDFSLFDVVLKNRKQRPAAVQTEEQYRFLYHTVAQMFCST----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84; Gaps
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19.2%; Score 465; DB 1; Length 631;
Best Local Similarity 30.9%; Pred. No. 8e-34;
Matches 126; Conservative 62; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Freeman Jr., Robert M.
APPLICANT: Plutaky, Jorge
APPLICANT: Neel, Benjamin G.
APPLICANT: Rosenberg, Robert D.
TITLE OF INVENTION: IDENTIFICATION OF NOVEL TYROSINE
TITLE OF INVENTION: PHOSPHATASES HAVING SH2 DOWAINS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                        ::||
527 QSQKGQESEYGNITYPPAMKNAHAKASRTSSKHKEDVYEN 566
                                                                                                                                                                                                 -----LQNA-----SPHYQNIKEN 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,389
FILING DATE: 28-FEB-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: BIH92-05MA
TELECOMMUNICATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,926
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/829,141
FILING DATE: 31-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/829,141
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/721,112
FILING DATE: 26-UN-1991
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08202389
Patent No. 5536536
GENERAL INFORMATION:
APPLICANT: Freeman Jr., Robert N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (617) 861-624
TELEPAX: (617) 861-624
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 631 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Two Mil:
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TY
US-08-202-389-8
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Search completed: August 17, 2004, 20:45:05 Job time : 20 secs

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NAYLOT, OLIVER
Kharitonenkov, Alexei Igorevich
TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDP1, CLK,
AND SIRP POLYPEPTIDES AND RELATED
PRODUCTS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS S.O
SOFTWARE: FastSEO for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/087,993
FILING DATE: 05-Mar-2002
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/877,150
FILING DATE: June 17, 1997
APPLICATION NUMBER: US. 60/019,629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                        August 17, 2004, 20:44:11; Search time 47 Seconds (without alignments) 3059.120 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                   US-10-087-993A-36
2424
1 MSRSLDSARSFLERLEARGG......NLRIGRPKGPRDPPAEWTRV 458
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| cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1292805 seqs, 313927144 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                               Run on:
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		Description	Sequence 36, Appl	Sequence 7, Appli	Sequence 32, Appl	Sequence 18, Appl	Sequence 95, Appl	Sequence 5, Appli	Sequence 2, Appli	Seguence 69, Appl	Sequence 71, Appl	Sequence 4, Appli	Sequence 848, App	Sequence 2, Appli	Sequence 845, App	Seguence 77, Appl	Sequence 75, Appl
SUMMARIES		. QI	US-10-087-993-36	US-10-243-687-7	US-10-087-993-32	US-09-822-295-18	US-10-366-547-95	US-10-309-423-5	US-09-822-295-2	US-10-366-547-69	US-10-366-547-71	US-10-309-423-4	US-10-322-281-848	US-10-309-423-2	US-10-322-281-845	US-10-366-547-77	US-10-366-547-75
		DB	13	14	13	σ	15	15	σ	15	15	15	16	15	16	15	15
		Query Match Length DB	458	453	448	802	802	802	807	780	780	692	778	808	773	382	775
	æ	Query Match	100.0	72.4	71.1	31.2	31.2	31.2	30.0	29.5	29.5	29.5	29.5	29.5	29.1	29.1	29.0
		Score	2424	1754.5	1724.5	755.5	755.5	755.5	727.5	709	709	708	708	708	706	705.5	703
		Result No.		2	m	4	Ŋ	9	7	α	σ	10	11	12	13	14	15

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18	N	Ξ.	235	12	-10-218-779-9	9
19	523	-	235	12	-012 - 8	8
20	21.	-	263	12	-10-087-684-93	9
2 2	21.		263	12	-10-218-779-	
22	96	ó	264	14	-10-245-539-6	ø
23	6	c	313	σ	-788-626-1	quence 17,
24	91.		1093	4	245-539-	Seguence 4
25	91.	0	1118	4	245-539-	ุผ
26	91.		1118	4	245-539-	
27	2	σ,	613	ູທ	366-547-	9
28	63.	6	341		88-626-2	23
29	46	O)	595		US-09-920-021A-1	e 1,
30	463	σ.	595	เก	366-547-8	60
31	463	φ.	595	LC)	366-547-	Sequence 91, Appl
32	463	σ.	597	LO.	366-547-89	œ
33	463	φ.	621	LO.	264-049-3	ĕ
34	463	φ.	843	4	072-036-11	Ξ
35	463	6	853	4	072-036-11	급
36	458	ω,	593	4	262-5	ď
37	458	ω,	593	ഹ	366-5	3
38	458	18.9	593	16	ä	ď
39	456	ω,	322	σ	-09-788-62	14,
40	454	œ	325	0	-62	E,
41	453	ω,	593	σ	-09-920-02	ñ
42	453		593	15	3-10-366-547-2	5
43	453	œ	593	15	66-547-	equence 3(
44	453		593	15	66-547-3	
4.5	453	18.7	593	16	-10-444-795B-	equence 7
					ALIGNMENTS	
RESULT 1	,					
Sequence; Publicat:	Sequence 36, App Publication No.	Applica	ion U 20169	/10 03A	087993 1	
 ando	GENERAL INFORMATION APPLICANT: Ull	NAT: Ul	JON: Ullrich, Axel	Axe		
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		<b>3</b> ₹	Wang, Hong	۵. ز ۲	Yang	
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                                                                           Suite 4700
               CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon &
STREET: 633 West F
                                                                                                              fornia
                                                                                           CITY: Los Angeles
STATE: California
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 67-3510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 TVDYVRQLLLITQMIPPDFSLFDVVLKWRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHYQNIKENCAPLYDDALFLRIPQALLAIPRPPGGVLRSISVPGSPGHAMADTYAEEQKR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGGGRTGVLC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAPAGAGSGTOTGTGARSAEEAPLYSKVTPRAORPGAHAEDARGTLPGRVPADOSPAG 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWINEDIMLRTLKVTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 2424; DB 13; Length 458; Best Local Similarity 100.0%; Pred. No. 1.8e-199; Matches 458; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7-0-7.
Sequence 10. US20030073120A1
Publication No. US20030073120A1
GENERAL INFORMATION:
APPLICANT: Aoki, Nachito
TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
AND RELATED PRODUCTS AND METHODS
APPLICATION NUMBER: U.S. 60/023,485
FILING DATE: August 9, 1996
FILING DATE: August 9, 1996
FILING DATE: NO. US20020169303A1ember 13, 1996
FILING DATE: No. US20020169303A1ember 13, 1996
FILING DATE: December 19, 1996
FILING DATE: DATE: U.S. 60/030,964
FILING DATE: NO. US20020169303A1ember 15, 1996
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                                                                                                                                                                                    NAME: Warburg, Richard J.
REGISCHATION VUMBER: 32,327
REFERENCE/DOCKET NUMBER: 225/298
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear;
HOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-087-993-36
                                                                                                                                                                                                                                                         TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELER: 67-3510
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                 LENGTH: 458 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                   FILING DATE: NO. US200 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RYKDVLPYDQTRVILSLLQBEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 14; Length 453;
                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/243,687
FILING DATE: 16-Sep-2002
CLASSIFICATION: CURKOWN>
PRIOR APPLICATION DATE: 29-Oct-1999
FILING DATE: 29-Oct-1999
APPLICATION NUMBER: 08/951,260
FILING DATE: 80-Oct-06-16, 1997
APPLICATION NUMBER: 06/030,860
FILING DATE: NO. US20030073120A1ember 13, 1996
FILING DATE: NO. US20030073120A1ember 13, 1996
FILING DATE: June 17, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Best Local Similarity 74.5%; Pred. No. 5.9e-142;
Matches 342; Conservative 37; Mismatches 73;
                                                                                                  COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Wazburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 227/004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-243-687-7
Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 453 amino acids
TYPE: amino acid
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Gaps

9 9 120 120 180 240 240 300 360

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241 AVDYVROLLITOTIPPNFSLFEVVLEWRKQRPAAVQTEEQYRFLYHTVAQLFSRTLQNNS 300
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                                                                                                                                                                                  1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 QKESRPVHQLQYMSWPDHGVPSSSDHILTMVEEARCLQGLGPGPLCVHCSAGGGRIGVLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLP-GRVPADQSPA
                                                                                                                                                                                                                                                                                                                 61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGFLPHTLLDFWRLVW
                                                                                                                                                                                                                                                                                                                                                                                                                                              BEGVKVIIMACREIENGRKRCERYWAQEQEPLOTGLFCITLIKEKWINEDIMLRTLKVTF
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                                                            DB 13; Length 448;
                                                         71.1%; Score 1724.5; DB 13; Lengt 74.2%; Pred. No. 2.2e-139; ive 37; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    420 GSGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPA 453
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM F.C. DOS 5.0
SOFTWARE: FRAESEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/822,295
FILING DATE: 02-Apr-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/081,345
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gregory D. Plowman
TITLE OF INVENTION: DIAGNOSIS AND
PTP04 RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/09822295
Patent No. US20020119501A1
GENERAL INFORMATION:
APPLICANT: Banija Jallal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      storage
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STATE: California
COUNTRY: U.S.A.
                                                               Query Match
Best Local Similarity 74.2 Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-09-822-295-18
US-10-087-993-32
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                                    361 GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLP-GRVPADQSPA 419
                                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/877,150

TILING DATE: JUNE 17, 1997

APPLICATION NUMBER: U.S. 66/019,629

FILING DATE: JUNE 17, 1996

APPLICATION NUMBER: U.S. 60/023,485

FILING DATE: AUGUST 9, 1996

APPLICATION NUMBER: U.S. 60/030,860

FILING DATE: NO. US20020163303Alember 13, 1996

APPLICATION NUMBER: U.S. 60/034,286

FILING DATE: December 19, 1996

APPLICATION NUMBER: U.S. 60/030,964

FILING DATE: NO. US20020163303Alember 15, 1996

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Naylor, Oliver
Kharitonenkov, Alexei Igorevich
TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDP1, CLK,
AND SIRP POLYPEPTIDES AND RELATED
PRODUCTS AND METHODS
                                                                                                                                                             420 GSGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
                                                                                                                                                                                                      415 GPDAYEEVTDGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Fast SEQ for Windows 2.0
RRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/087,993
FILING DATE: 05-Mar-2002
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 225/298
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES.
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
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TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                           RESUL: 3
US-10-08-93-32
| US-10-08-93-32 |
| US-10-08-08-32, Application US/10087993 |
| Publication No. US20020169303A1 |
| GENERAL INFORMATION: |
| APPLICANT: Ullrich, Axel |
| APPLICANT: Weng Woong |
| Kim, Yeong Woong |
| Chen, Zhengjun Chen, Zhengjun |
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TELEX: 67-310
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 453 amino acids
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27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY
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Publication No. US20040006777A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mus musculus US-10-309-423-5
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Best Local Simil
Matches 161; C
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US-10-309-423-5
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                                                                                                                                                                                                                                                                                                                                               ASEFLKLKRQSTKYKADKIYPTTVAQRPKNIKKKNIKPYKDILPYDHSLVELSLLTSDEDSSY
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Publication No. US20030215899A1

GENERAL INFORMATION:
APPLICANT: Meng, Tzu-Ching
APPLICANT: Torks, Nicholas K.
TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
TITLE OF INVENTION: PHOSEPHARASES
FILE REFERENCE: 200125,439
CURRENT APPLICATION NUMBER: US/10/366,547
CURRENT FILING DATE: 2003-02-12
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 95
LENGTH: 802
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                                                                                                                                                                                                                                                         Length 802;
                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                       Query Match 31.2%; Score 755.5; DB 9; Best Local Similarity 44.0%; Pred. No. 9.2e-56; Matches 161; Conservative 55; Mismatches 119;
     REFERENCE/DOCKET NUMBER: 234/253
                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                TELEX: 67-3510
INFORMATION FOR SEQ 1D NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 802 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-366-547-95
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Best Local
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                                                                                                                                                                                 205
                                                                                                                                                                                                                                                                                                       206 HMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 265
                                                                                                                                                                                                                                                                                                                                      26 KWRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPHYQNIKENCAPLYDDALFLRTPQA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                            205
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                                                                                                                                                                                                                          147 QEQE-PLOTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLAIPRPPGGVLRSISVPGS-----PGHAMAD--TYAEEQKRGAPAGAGSGTQTGTGTG
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25 ASEFLKLKRQSTKYKADKIYPTTVAQRPKNIKKNRYKDILPYDHSLVELSLLTSDEDSSY
                                                            87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HSC Research and Development Limited Partnership TITLE OF INVENTION: Human Lymphoid Protein Tyrosine Phosphatasses FILE REPERENCE: 92906-2 CURRENT APPLICATION WHERE: US/10/309,423 CURRENT APPLICATION WHERE: US/00/600,358 PRIOR PELING DATE: 2002-12-03 PRIOR PILING DATE: 2000-09-25 PRIOR PILING DATE: 1998-01-16 NUMBER OF SEQ ID NOS: 7 SOFTWARE PLANG DATE: 1998-01-16 SEQ ID NOS: 7 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.2%; Score 755.5; DB 15; Length Similarity 44.0%; Pred. No. 9.2e-56; Conservative 55; Mismatches 119; Indels
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145 BPGEMQLEPGPFSVSCEAEK-RKSDYIIRTLKVKFNSETRIIYQFHYKXWWPDHDVPSSID 203
                                                           206 HMLAMVEBARRLQGSGPEPLCVHCSAGGGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 265
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                                                                                    DVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFG
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                                                                                                                                         266 KWRKORPAAVOTEEOYRFLYHTVAOMF---CSTLONASPHYONIKENCAP 312
                                                                                                                                                              26;
                                                                                                                                                                                                                                        RESULT 8
US.10-366-547-69
i Sequence 69, Application US/10366547
; Publication No. US20330215899A1
; GENERAL INFORMATION:
APPLICANT: Mong, Tzu-Ching
; APPLICANT: Tonke, Nicholas K.
APPLICANT: Cool, Deborah E.
TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
TITLE OF INVENTION: BUOSPHATASES
; CURRENT APPLICATION NUMBER: US/10/366,547
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 69
; SEQ ID NO 69
; SEQ ID NO 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 780;
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US-10-366-547-71

US-10-366-547-71

Sequence 71, Application US/10366547

Publication No. US20030215899A1

GENERAL INFORMATION:

APPLICANT: Meng, Tzu-Ching

APPLICANT: Tonks, Nicholas K.

APPLICANT: Tonks, Nicholas K.

APPLICANT: Cool, Deborah E.

7 TITLE OF INVENTION: PHOSPHATASES

7 TITLE OF INVENTION: PHOSPHATASES

7 FILE REFERENCE: 200125.439
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29.2%; Score 709; DB 15; 1
Best Local Similarity 41.0%; Pred. No. 8.8e-52;
Matches 144; Conservative 65; Mismatches 116;
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CORGANISM: Homo sapiens
US-10-366-547-69
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      308
                                            326 LLAIPRPPGGVLRSISVPGS-----PGHAMAD--TYAEEQKRGAPAGAGSGTQTGTG 377
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        --KRHMDVISDNHLG
                                                                                                                                                                                                                                                                                                                APLICANT: Bahija Jallal
APPLICANT: Bahija Jallal
Gregory D. Plowman
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
PPPO4 RELATED DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch 30.0%; Score 727.5; DB 9; al Similarity 46.9%; Pred. No. 2.4e-53; 136; Conservative 56; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/822,295
FILING DATE: 02-Apr-2001
CLASSIFICATION: Chiknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATPLICATION NUMBER: 09/081,345
FILING DATE: <unknown>
ATPLICATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 234/253
TELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-0440
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TELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-0440
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ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
      264 EMRTQRPSLVQTQEQYELVYSAVLELF-
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;
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-822-295-2
                                                                                                                                                                                                                                                               Sequence 2, Application US/09822295
Patent No. US20020119501A1
GENERAL INFORMATION:
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                363 TMNAÈE 368
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US-09-822-295-2
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Best Local Si
Matches 136;
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147 QEQE-PLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD 205
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Best Local Similarity
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US-10-309-423-2
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| CUIIVMACREFEMGRKKCERYWPLYGEDPITFAPFKIS-CEDEQARTDYFIRTLLLEFQN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 ESRRLYQFHYVNWPDHDVPSSFDSILDMISLARKYQEHEDVPICIHCSAGCGRTGAICAI 244
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                                                                                                                                                                                                                                                                                                                               64 DVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFG 123
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                                                                                                                                                                                                                       Gaps
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Publication No. US200400677741

GENERAL INFORMATION:

APPLICANT: HSC Research and Development Limited Partnership

TITLE OF INVENTION: Human Lymphoid Protein Tyrosine Phosphatases

FILE REFERENCE: 92906-2

CURRENT PPLICATION NUMBER: US/10/309,423

CURRENT FILING DATE: 2000-12-03

PRIOR PLICATION NUMBER: US/09/600,358

PRIOR PLICATION NUMBER: CA 2.220,853

PRIOR APPLICATION NUMBER: CA 2.220,853

PRIOR FILING DATE: 1998-01-16

NUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENTH: 692
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                                                                                                                                                                                   Length 780;
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                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                     66; Mismatches 116;
                                                                                                                                                                                   Query Match

29.2%; Score 709; DB 15;
Best Local Similarity 40.7%; Pred. No. 8.8e-52;
Matches 143; Conservative 66; Mismatches 116;
CURRENT APPLICATION NUMBER: US/10/366,547
CURRENT FILING DATE: 2003-02-12
NUMBER OF SEQ ID NOS: 98
SEQ TWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 71
LENGTH: 780
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Best Local Similarity 46.7%
Matches 136; Conservative
                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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126 VVIIVMACREFEMGRKKCERYWPLYGEDPITFAPFKIS-CEDEQARTDYFIRTLLLEFQN 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 DILPFDHSRVKLTLKTPSQDSDYINANFIKGVYGPKAYVATQGPLANTVIDFWRMIWEYN 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYK
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                                                                                                                                                                                              265 LIMRKQRPAAVQTEEQYRFLYHTVAQMF---CSTLQNASPHYQNIKENCAP 312
                                                                                                                                                                                                                                     303 YQNIKENCAPLYDDALFLRTPQALLAI-----PRPPGGVLRSISVPG 344
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Sequence 2, Application US/10309423

CENEAL INFORMATION: US20040006777A1

APPLICANT: HSC Research and Development Limited Partnership

TITLE OF INVENTION: Human Lymphoid Protein Tyrosine Phosphatases

TITLE OF INVENTE: 929066-2

CURRENT APPLICATION NUMBER: US/10/309,423

PRIOR APPLICATION NUMBER: US/209/600,358

PRIOR PLING DATE: 2000-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 778;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 848, Application US/10322281
Publication No. US20040126762A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: More S. Malandro
FILE REPERENCE: 25452001000
CURRENT FILING DATE: 2002-12-17
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.2%; Score 708; DB 16;
40.7%; Pred. No. 1.1e-51;
iive 66; Mismatches 116;
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303
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                                                                                                                                                                                                                      365 LTPSPPSAFPTVTTVWQDSDRYHPKPVLHMDEQHPADLNRSYDKSADPMGKSESAIEHID 424
                                                                                                                                                                                                                                                                                                425 KKLERNLSFEIKKVPLQEGPKSFDGNTLLNRGHAIKIKSASSSVVDRTSKPQELSAGALK 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                           545 VPDSPDGKSPDNHSQTLKTVSSTPNSTÅEBEAHDLTEHHNSSPLLKAPLSFTNPLHSDDS 604
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                                          605 DSDGGSSDGAVTRNKTSISTASATVSPASSAESACTRRVLPMSIARQEVAGTPHSGAEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       665 ADVSESPPPLPERTPESFVLADMPVRPEWHELPNQEWSEQRESEGLTTSGNEKHDAGGI
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                                                                                                  ---STLONASPH----
                                                                                                                                        GAQKIADGNEITTGTMVSSIDSEKQDSPPPKPPRTRSCLVEGDAKEEILQPPEPHPVPPI
                                                                                                                                                                                                                                                                                                                                                                            485 VDDVSQNSCADCSAAHSHRAAESSEESQSNSHTPPRPDCLPLDKKGHVTWSLHGPENATP
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45.1%; Pred. No. 6.5e-52;
iive 59; Mismatches 94;
                                                                                                                                                                                                                                                            304 QNIKENCA-----PL-----YDDALFL-----
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Publication No. US20030215899A1
GENERAL INFORMATION:
APPLICANT: Meng, Tzu-Ching
APPLICANT: Tonks, Nicholas K.
APPLICANT: Cool, Deborah E.
TITLE OF INVENTION: REVERSIBLE OXIDATION OF PRC;
TITLE OF INVENTION: PHOSPHATASES
FILE REFERENCE: 200125.439
CURRENT APPLICATION NUMBER: US/10/366,547
CURRENT APPLICATION NUMBER: 2003-02-12
NUMBER OF SEQ ID NOS: 98
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PastSEQ for Windows Version 4.0
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TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-366-547-77
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Best Local Similarity 45.1<sup>s</sup>
Matches 133; Conservative
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US-10-366-547-77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 HMLAMVEBARRLQGSGPEPLCVHCSAGCGRTGVLCT-VDYVRQLLLTQMIPPDFSLFDVV 264
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                                                                                                                                                                                                                                                                               27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.1%; Score 706; DB 16; Length 773;
25.5%; Pred. No. 1.6e-51;
.ive 86; Mismatches 163; Indels 324;
                                                                                                                                                                                                                                         9
                                                                                                                                                                                                 Length 808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 529452001000
CURRENT PEPLICATION WUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 845
LENGTH: 773
                                                                                                                                                                                                                                         95; Indels
                                                                                                                                                                                                 ; DB 15;
1.1e-51;
                                                                                                                                                                                               29.2%; Score 708; DB 46.7%; Pred. No. 1.1e ive 54; Mismatches
    2,220,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 845, Application US/10322281; Publication No. US20040126762A1; GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: CA 2
PRIOR FILING DATE: 1998-01-16
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 25.5%
Matches 196; Conservative
                                                                                                                                                                                               Query Match
Best Local Similarity 46.7
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Mus musculus
US-10-322-281-845
                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-10-322-281-845
                                                                                                                                            ; ORGANISM: Ho
US-10-309-423-2
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LLEFON 184  GVLCTV 242  OV 361	244 Db	297 299 Qy	<b>a</b>	Qy 414		Search completed: Aug Job time : 50 secs					Gaps 17;		LVWEFG 123 ::  : MIWEYN 125	KVTFQK 182 :		GAICAI 244 Q 297	QLYBIH 304		HPVPPI 364				
VVIIVMACREFEMGRKKCERYWPLYGEDPITFABPKISCENEQ-ARTDYFIRTLLLEFQN ESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGGGRTGVLCTV 	ESRRLYQFHYVNWPPHDVBSSFDSTLDMISLMRKYQEHEDVPICIHCSAGCGRTGAICAI	DYYROLLITOMIPPDESLEDVVLKMRKORÞANQTESQYRFLYHYVAQMFCSTLO DYTWNLLKAGKIPEERVVFNLIOEMRYQRHSANQTKEOYBLVHRAIAQLFEKQLO		75	APPINCALLON US/1036634/ No. US/20030215899Al RMATION:	Meng, Tzu-Ching Tonks, Nicholas K.	COOL, DEBOTAN ENTRY OXIDATION OF PROTEIN TYROSINE VENTION: PHOSPHATASES	; FILE REFERENCE: 200125.439 ; CURRENT APPLICATION NUMBER: US/10/366,547 ; CURRENT FILING DATE: 2003-02-12	NUMBER OF SEQ ID NOS: 98 SOFTWARE: FastSEQ for Windows Version 4.0 EQ ID NO 75	LENGTH: 775 TYPE: PRT ORGANISM: Mus. musculus 0-366-547-75	29.0%; Score 703; DB 15; Length 775; 25.0%; Pred. No. 2.9e-51; vative 84; Mismatches 162; Indels 336;	RSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYK     : :   :	DVLPYDQTRVILSLLQBEGHSDYINGNFIRGYDGSLAYIATQGPLPHTLLDFWRLVWEFG	VKVILMACREIENGRKRCERYW-AQEQEPLQTGLFCITLIKEKWINEDIMLRTLKVTFQK	ESRSUYQLQYMSWPDRGVPSSPDHMLAMVEBARRLQGSGPBPLCVHCSAGCGRTGVLCTV	ESRRLYQFHYVNWPDHDVPSSFDSILDMISLMRKYQEHEDVPICIHCSAGGGRTG* DYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQ-			GAQKIRDGNEITTGTMVSSIDSEKQDSPPRPPRTRSCLVEGDAKEEILQPPEPHPVPPI	GAQKIRDGNEITTGTMVSSIDSEKQDSPPRRPRTRSCLVBGDAKBEILQPPEPH NASP	GAQKIRDGNEITTGTMVSSIDSEKQDSPPRPRPRSCLVGGDAKEEILQPPEPHPVPPI NASP LTPSPPSAFPTVTTVWQDSDRYHPKPVLHMASPEQHPADLANGYDKSADQWGKSESAIEH	LOP DOW	GAQKIRDGNEITTGTWVSSIDSEKQDSPPKPPRTRSCLVEGDAKEEILQPPEPH
Db 126 Qy 183		Oy 243 Db 245		RESULT 15 US-10-366-547-	<pre>/ Sequence /s, Applica / Publication No. US20 / GENERAL INFORMATION:</pre>	APPLICANT:	; AFFLICANT: ; TITLE OF IN ; TITLE OF IN	; FILE REFERE ; CURRENT APF ; CURRENT FIL	; NUMBER OF SE( ; SOFTWARE: Fat ; SEQ ID NO 75	; LENGTH: 775 ; TYPE: PRT ; ORGANISM: Mu US-10-366-547-75	Query Match Best Local Similarity Matches 194; Conser	Oy 9 Db 8	Qy 64 Db 66	Qy 124 Db 126		Db 185 Qy 243	Db 245	Qy 298	305 a05				

Search completed: August 17, 2004, 20:50:05

us-10-087-993a-36.rpr

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GenCore version 5.1.6
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                  Copyright
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protein search, using sw model ı OM protein August 17, 2004, 20:40:39; Search time 17 Seconds (without alignments) 2591.513 Million cell updates/sec Run on:

US-10-087-993A-36 2424 Title:

1 MSRSLDSARSFLERLEARGG.......ALRIGRPKGPRDPPAEWTRV 458 Perfect score:

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

of hits satisfying chosen parameters: Total number

283366 segs, 96191526 residues

Searched:

length: 0 length: 2000000000 sed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

Database

PIR\_78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

protein tyrosine p protein-tyrosine-p protein-tyrosine-p JH0609 JC1368 S48748 S55345 A49724 A44390 A55148 S200828 S200828 JNO805 JNO805 JG5167 A53593 A53593 A53593 A53593 A53593 A53503 T198716 T28401 T19631 T19 B Length Result

protein-tyrosine-p protein-tyrosine-p	protein-tyrosine-p HPTP beta-like tyr	procein-tyrosine-p protein-tyrosine-p probable protein-t	leukocyte antigen- receptor tyrosine	protein-tyrosine-p protein-tyrosine-p	protein-tyrosine-p protein-tyrosine-p	protein-tyrosine-p protein-tyrosine-p	leukocyte antigen-
A41622 A47373	JH0692 S68700	16/530 167629 T43148	S46216 T30938	A57064 S60613	S12050 B48148	A48148 I49372	TDHULK
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1301 829	360 1238	2466 1200	1898	1188 1216	1997	1445	1897
17.5	17.5	17.4	17.3	17.3	17.3	17.3	17.3
424 423.5	421.5	421.5 421.5 421	4 2 0 4 2 0	419.5 419.5	419.5 419	419	418.5
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protein-tyrosine-phosphatase (BC 3.1.3.48) PEP, nonreceptor type 8 - mouse N.Alternate names: protein-tyrosine-phosphatase PEP Cippedies: Mis musculus (house mouse).
Cipate: 03-May-1994 #sequence revision 26-May-1994 #text\_change 11-Jun-1999 C;Accession: B44390; S71952; \$Z7876
R Matchlews, R.J.; Bowne, D.B.; Flores, E.; Thomas, M.L.
Mol. Call. Biol. 12, 2396-2405, 1992
A;Title: Characterization of hematopoietic intracellular protein tyrosine phosphatases: 
A,Title: Characterization of hematopoietic intracellular protein tyrosine phosphatases: A,Reference number: A44390; MUID:92236615; PMID:1373816
A;Accession: B44390
A;Rolecule type: man.AA
A;Residues: 1-802 - AAT>
A;Cross-references: GB:M90388; NID:g200522; PIDN:AAA39994.1; PID:g200523
R;Cloutier: AF: Velletter, A.
EMBO J. 15, 4909-4918, 1996
A;Title: Association of inhibitory tyrosine protein kinase p50(csk) with protein tyrosine A; Ancesion: G1052; MUID:97045099; PMID:8890164

A)Gene: 70zpep C;Complex: physically associates with inhibitory tyrosine protein kinase Csk; interaction C;Punction: C;Punction: probably an effector and/or regulator of tyrosine protein kinase csk in T-C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 8; protein-tyrosine-phosphi C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase F;54-278/Domain: protein-tyrosine-phosphatase homology <PTP> F;497-802/Region: glutamic acid/proline/serine/threonine-rich F;688-659/Region: proline-rich F;688-659/Region: proline-rich F;227/Active site: Cys (phosphocysteine intermediate) #status predicted F;237/Binding site: substrate phosphate (Arg) #status predicted AjAccession: S71952
AjStatus: mucleic acid sequence not shown; not compared with conceptual translation
AjMolecule type: mRNA
AjRolecules: 495-789 <CLO>
CjComment: This protein is found primarily in hematopoietic tissues.
CjGenetics:
AjGene: 702pep
CjComplex: physically associates with inhibitory tyrosine protein kinase Csk; interaction CjFunction:

31.2%; Score 755.5; DB 1; Length 802; 44.0%; Pred. No. 2e-47; ive 55; Mismatches 119; Indels 31; Gaps Local Similarity 44.0 tes 161; Conservative

7;

86 25 ASEPLKIKRQSTKYKADKIYPTTVAQRPKNIKKARYKDILPYDHSLVELSLLTSDEDSSY 27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY ò g

87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIBNGRKRCERYWA 셤 à

147 QEQE-PLQTGLFCITLIKEKWINEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD 205

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protein-tyrosine-p probable protein-t protein-tyrosine-p

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protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN12, nonreceptor type 12 [validated] - hume N.Alternate names: PTP-PEST; PTPG1 C.5pecies: Homo sapiens (man) (c.5pecies: Homo sapiens (man) (c.5pecies: Homo sapiens (man) (c.5pecies: 30-Sep-1993 #sequence revision 01-Mar-1996 #text_change 21-Jun-2002 C.7accession. JC1368, A47506, A45496; S41746 #text_change 21-Jun-2002 B.5chem. Biophys. Res. Commun. 189; 1223-1230, 1992 A.7Ttle: Cloning and characterization of a human cDNA encoding a novel putative cytoplass A.7ttle: Cloning and characterization of a human cDNA encoding a novel putative cytoplass A.7Accession: JC1368, MUID:93112015; PMID:1472029
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                                                                                                                                                                                                                124 VKVILMACREIENGRKRCERYW-AQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQK 182
                                                                                                                                                                                                                                                                                 126 VVMIVNACREFEMGRKKCERYWPLYGEDPITFRAPFKISCENEQ-ARTDYFIRTLLLEFQN 184
                                                                                                                                                                                                                                                                                                                                                                                                      305 EHRRSVMVMKLPLELWSVPLIARRDLSAKAAADSKLPCRRGCOGRNTTATRTSPGATHPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           365 AITSFSLPNVTTVCRTVTGTTQSQCCTWPHQSNTQPTSTEAMINQRTNGAKSESAIEHID
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RRFIQRVQAMKSPDHNGEDN--FARDFWRLRRLSTKYRTEKIYPTATGEKEENVKKNRYK
                                                                                                                     485 VDDVSQNSCADCSAAHSHRAAESSEESQSNSHTPPRPDCLPLDKKGHVTWSLHGPENATP
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A, Residues: 1-780 c TAK.
A, Residues: 1-780 c TAK.
A, Cross-references: DDBS:D13380; NID:9220033; PIDN:BAA02648.1; PID:9220034
A, Note: the authors translated the codon AGT for residue 636 as Ala
A, Note: the authors translated the codon AGT for residue 636 as Ala
A, Note: the authors translated the codon AGT for residue 636 as Ala
A, Note: the authors translated the codon AGT for residue 636 as Ala
A, Radge, O.; Co., D.; Sommercorn, J.; Tonks, N.K.
A, Reference number: A47506; MUID:93352561; PMID:8349645
                                                                        DVLPYDQTRVILSLLQBEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFG
                                                                                                                                                                                                                                                                                                                                                             183 ESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTV
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A;Accession: A47506
A;Molecule type: mRNA
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A;Status: not compared with conceptual translation
A;Molecule type: mRNA
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A;Molecule type: mRNA
C;Comment: This protein tryrosine-phosphatase, nonreceptor type 12; protein-tyrosine-phosp
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 12; protein-tyrosine-phosp
C;Moywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
F;55-299/Domain: protein-tyrosine-phosphatase homology c*PPP
F;231/Active site: Cyc (phosphocysteine intermediate) #status predicted
F;231/Active site: substrate phosphate (Arg) #status predicted
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       BEGETOLOFGEPSISCEAEK-KKSDYKIRTLKAKFNNETRIIYQFHYKNWPDHDVPSSID 203
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                                                                                                                                                               206 HMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL
                                                                                                                                                                                                                                                              KARKORPAAVOTEEOYRFLYHTVAOMFCSTLONASPHYONIKENCAPLYDDALFLRTPQA
                                                                                                                                                                                                                                                                                                                                  264 EMRIQRPSIVQIQEQYELVYSAVLELF-----KRHMDVİSDNHLG------REIQA
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A;Residues: 88-91,'G',93-110,'G',112-118,'S',120,'T',122 <DE2>
A;Experimental source: embryonic carcinoma cell, P19 cell, clone
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Matches 195; Conservative
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pe 12; protein-tyrosine-phospł tyrosine-specific phosphatase

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C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 12; protein C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-spe F;58-282/Domain: protein-tyrosine-phosphatase homology PTP-F;211/Active site: Cys (phosphocysteine intermediate) #status predicted F;237/Binding site: substrate phosphate (Arg) #status predicted
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A Characterial Tyll.23-741.23
C; Map possition: 741.23-741.23
C; Map possition: 741.23-741.23
C; Map possition: 741.23-741.23
C; Map possition: protein-tyrosine-phosphatase, nonreceptor type 12; protein-tyrosine-phosp C; Meywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase P; 58-282/Domain: protein-tyrosine-phosphatase homology, PPTP-
E; 231/Active site: Cys (phosphorysteine intermediate) #status predicted
F; 231/Active site: substrate phosphate (Arg) #status predicted
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A; Residues: 1-120, I', 122-321, I', 323-780 <YAN>
A; Cross-references: EMBL.M93455; NID:g222408; PIDN:AAA36529.1; PID:g222409
R; Yang, Q.; Co, D.; Sommercorn, J.; Tonks, N.K.
J. Biol. Chem. 268, 6622-6628, 1993
A; Title: Cloning and expression of PTP-PEST. A novel, human, nontransmembrane protein t A; Reference number: A45496; MUID:93203262; PMID:8454633
A; Title: Cloning and expression of PTP-PEST. A novel, human, nontransmembrane protein t A; Reference number: A45496
A; Molecule type: mRNA
A; Residues: 1-120, I', 122-321, I', 323-494, 518-525, FLLMRKDM' <YA2>
A; Molecule extracted from NCBI backbone (NCBIN:127946)
A; Note: sequence extracted from NCBI backbone (NCBIN:127945)
A; Note: sequence as been revised in reference A47506
R; Takekawa, M.; Itoh, F.; Hinoda, Y.; Adachi, M.; Ariyama, T.; Inazawa, J.; Imai, K.; Y FEBS Lett. 339, 222-228, 1994
A; Title: Chromosomal localization of the protein tyrosine phosphatase G1 gene and chara A; Reference number: S41746; MUID:94156037; PMID:7509295
                                                                                                                                  nontransmembrane protein
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A;Residues: 59-127, YY',130-134,'TE' <TA2>
A;Note: sequence shown is wild type
C;Comment: PEST sequences in this widely expressed protein suggest that
C;Genetics:
A;Gene: GDB:PTPN12
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64 DVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFG
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RESULT 4
848748
protein-tyrosine-phosphatase (EC 3.1.3.48), probable nonreceptor type 12 splice form - r
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: $48748
R;Moriyama, T.; Kawanishi, S.; Inoue, T.; Imai, E.; Kaneko, T.; Xia, C.; Takenaka, M.; N
FEBS Lett. 353, 305-308, 1994
A;Title: cDNA cloning of a cytosolic protein tyrosine phosphatase (RKPTP) from rat kidne
A;Reference number: $48748; MUID:95046282; PMID:7957881
                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-382 <MOR>
A;Cross-references: GB:D38072; NID:g567262; PIDN:BAA07266.1; PID:g699627
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123

63

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;Map position: 5A3-B
;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 12; protein-tyrosine-phosph;Superfamily: protein-tyrosine-phosphoric monoester hydrolase; tyrosine-specific phosphatase;Sa282/Domain: protein-tyrosine-phosphatase homology <PTP>
;231/Active site: Cys (phosphocysteine intermediate) #status predicted
;237/Binding site: substrate phosphate (Arg) #status predicted
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C.Species: Mus musculus (house mouse)
C.Date: 10-Oct-1995 #sequence_revision 01-Nov-1996 #text_change 22-Jun-1999
C.Aocession: S5345; S24561; Iq8666
R.Chacesstan: S5345; S24561; Iq8666
R.Chacest. A.; Wagner, J.; Shen, S.H.; Tremblay, M.L.
Biochem. J. 308, 425-432, 1995
A.Aitle: Murine protein tyrosine phosphatase-PEST, a stable cytosolic protein tyrosine phaceston: S5345
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A.Molecule type: DNA
A.Residues: 1-775 CHA
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A.R
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                                                                                                                  9.
               DB 1; Length 382;
                                                                                                            Indels
Query Match
29.1%; Score 705.5; DB 1;
Best Local Similarity 45.1%; Pred. No. 3.6e-44;
Matches 133; Conservative 59; Mismatches 94;
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Best Local Similarity
Matches 194; Conserv
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Gaps

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A,Molecule type: mRNA
A,Residues: 1-595 cMAT-
A,Gross-references: GB:M90389; NID:g200550; PIDN:AAA40007.1; PID:g200551
A,Cross-references: GB:M90389; NID:g200550; PIDN:AAA40007.1; PID:g200551
R;Yi, T.L.; Cleveland, J.L.; Ihle, J.N.
R;Yi, T.L.; Cleveland, J. 136-846, 1992
A)Title: Protein tyrosine phosphatase containing SH2 domains: characterization, preferent
A,Reference number: A42031; MUID:92123209; PMID:1732748
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R;Shultz, L.D.; Schweitzer, P.A.; Rajan, T.V.; Yi, T.; Ihle, J.N.; Matthews, R.J.; Thomas
Cell 73, 1445-1454, 1993
                                                                                                                                                                                                                            F;846-1070/Domain: protein-tyrosine-phosphatase homology <PTP1>
735,78 83,107,132,149,122,165,203,286,324,323,325,376,333,401,436,439,470,490,558,57.
F;1022/Active site: Cys (Phosphocysteine intermediate) #status predicted
F;1028/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein-tyrosine-phosphatase (BC 3.1.3.48), nonreceptor type 6 - mouse NyAlternate names: hematopoietic cell phosphatase (HCP); protein-tyrosine-phosphatase IC (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (Spaces: Mus musculus (house mouse) (Spaces: Musculus (house mouse) (Spaces: Musculus (house mouse) (Spaces: Musculus May 1994 #sequence revision 19-May 1994 #text change 11-Jun-1999 (Spaces: Musculus May 1997 Matthews, R.J.; Bowne, D.B.; Flores, E.; Thomas, M.L. Moule (11, 2396-2405, 1992 Musculus Musculus protein tyrosine phosphatases: Canad threonine-rich sequences.
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A)Arores sequence extracted from NCBI backbone (NCBIN:76845, NCBIP:76846)
A)Arore: sequence extracted from NCBI backbone (NCBIN:76845, NCBIP:76846)
B)Ariore: A: Cleveland, J.L.; Ihle, J.N.
Blood 78, 2222-2228, 1991
Blood 78, 2222-2228, 1991
A)Aritle: Identification of novel protein tyrosine phosphatases of hematopoietic cells by A)Reference number: A61180; MUID:92032882; PMID:1932742
A)Accession: F61180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    957 MENWIVREILL--LQVEEQK-TLSVRQFHYQAWPDHGVPSSPDILLAFWRMLRQWLDQIM 1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1014 EGGPP---IVHCSAGVGRIGILIALDVILRQLQSEGLLGP----FSFVRKMRESRPLMVQ 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITL----I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        897 PLPQTVGDFWRLVWEQQSHTLVMLTNCMEAGRVKCEHYWPLDSQPCTHGHLRVTLVGEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 QGSGPEPLCVHCSAGCGRIGVLCTVD-YVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQ
                                                                                                                                                                                                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                                                                                      Length 1118;
F,205-289/Domain: fibronectin type III repeat homology <3FNC> P,296-379/Domain: fibronectin type III repeat homology <3FND> P,388-468/Domain: fibronectin type III repeat homology <3FND> P,474-558/Domain: fibronectin type III repeat homology <3FNE> P,564-658/Domain: fibronectin type III repeat homology <3FNE> P,564-658/Domain: fibronectin type III repeat homology <3FNF> P,767-737/Domain: fibronectin type III repeat homology <3FNF> P,762-778/Domain: fibronectin type III repeat homology <3FNF> P,779-1118/Domain: intracellular #status predicted <INN>
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A;Accession: A44390
                                                                                                                                                                                                                                                                                                                                                                   Query Match 20.3%; Score 491.5; DB 1; Best Local Similarity 43.3%; Pred. No. 6.6e-28; Matches 116; Conservative 36; Mismatches 91;
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A; Molecule type: mRNA
A; Residues: 1-595 < YIl>
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C;Species: 03-May-1994 #sequence_revision 23-Feb-1996 #text_change 16-Jun-2000
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                                            VKVILMACREIENGRKRCERYW-AQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQK 182
                                                                         --IPRP------PGGVLRSI-
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A;Residues: 1-1118 <MATO>
A;Cross-references: GB:D15049; NID:g475003; PIDN:BAA03645.1; PID:g475004
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A,Cross-references: GDB:305504
A,Map position: 19q13.4-19q13.4
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A; Reference number: 152816; MUID:93313972; PMID:8324828
A; Reference number: 152816; MUID:93313972; PMID:8324828
A; Reference number: 152816
A; Residues: preliminary; translated from GB/EMEL/DDBJ
A; Residues: greliminary; translated from GB/EMEL/DDBJ
A; Residues: 334-353, 359-382 <SHU1>
A; Residues: 334-353, 359-382 <SHU1>
A; Residues: 325-386; Ranslated from GB/EMEL/DDBJ
A; Accession: 152816
A; Residues: 350-358; Ranslated from GB/EMEL/DDBJ
A; Residues: 350-358; Ranslated from GB/EMEL/DDBJ
A; Residues: 350-358; Ranslated from GB/EMEL/DDBJ
A; Residues: 350-358; Ranslated from GB/EMEL/DDBJ
A; Residues: 347-6; VPREPHIWRAGGYRAAGGRALD' <SHU3>
A; Residues: 347-6; VPREPHIWRAGGYRAAGGCRALD' <SHU3>
A; Note: frameshift mutation
A; Ryenidues: 347-6; VPREPHIWRAGGYRAAGGCRALD' SHU3>
A; Note: frameshift mutation
A; Ryenidues: 347-6; VPREPHIWRAGGYRAAGGCRALD' SHU3>
A; Note: frameshift mutation
A; Ryenidues: 347-6; VPREPHIWRAGGYRAAGGCRALD' SHU3>
A; Note: frameshift mutation
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A; Note: frameshift mutation
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A; Ryenidues: 347-6; VPREPHIWRAGGCRALD' SHU3>
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19.6%; Score 475.5; DB 1; Length 595;
Best Local Similarity 36.2%; Pred. No. 4.4e-27;
Matches 106; Conservative 53; Mismatches 105; Indels 29
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C; paperses: Nature norregicus (Norway rac); C; paperses: Nature norregicus (Norway rac); C; paperses: Nature norregicus (Norway rac); C; paperses: Nature number: A55148 |
R; Mauro, L.J.; Olmsted, E.A.; Skrobacz, B.M.; Mourey, R.J.; Davis, A.R.; Dixon, J.E.
J. Biol. Chem. 269, 30659-30667, 1994
A; Title: Identification of a hormonally regulated protein tyrosine phosphatase associated A; A; Ctestion of a hormonally regulated protein tyrosine phosphatase associated A; A; Accession: A55148 | MUID:95074080; PMID:7527035 |
A; Accession: A55148 | MUID:95074080; PMID:7527035 |
A; Accession: A55148 | MUID:95074080; PMID:7527035 |
A; Accession: A55148 | MUID:95074080; PMID:7527035 |
A; Accession: A55148 | A; AMUA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: MPNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 OTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 ACREIENGRKRCERYWAQEQEPLQTGLFCITLIKE----KWLNEDIMLRTLKVTFQKESR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVYQLQYMSWPDRGVPSSPDHMLAMV----EEARRLQGSGPEPLCVHCSAGCGRTGVLCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 SFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
rotein-tyrosine-phosphatase (EC 3.1.3.48), receptor type OST precursor .
Alternate names: OST-PTP; osteotesticular protein-tyrosine-phosphatase .
Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
19.6%; Score 474; DB 1; Length 171
Best Local Similarity 39.9%; Pred. No. 2.2e-26;
Matches 114; Conservative 35; Mismatches 111; Indels
                      protein-tyrosine-phosphatase
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A,Status: nucleic acid sequence not shown A,Molecule type: mRNA
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                     A;Molecule type: mRNA
A;Residues: 1-85, VV, 87-595 <PLU>
A;Residues: 1-85, VV, 877-273; NID:g338079; PIDN:AAA36610.1; PID:g338080
A;Cross-references: GB:M7273; NID:g338079; PIDN:AAA36610.1; PID:g338080
A;Shen, S.H.; Bastien, L.; Posner, B.I.; Chretien, P.
Nature 353, 868, 1991
A;Title: Corrigendum: A protein-tyrosine phosphatase with sequence similarity to the SHZ
A;Reference number: S20825
A;Accession: S20825
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CySuperfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosph
CySuperfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosph
CySuperfamily: protein-tyrosine-phosphatase
CySuperfamily: SH2 homology <SH2A>
F;110-211/Domain: SH2 homology <SH2B>
F;265-521/Domain: phosphatase catalytic domain #status predicted <PHP>
F;270-504/Domain: protein-tyrosine-phosphatase homology <PTP>
F;270-504/Domain: protein-tyrosine-phosphatase homology <PTP>
F;453/Active site: Cys (phosphocysteine intermediate) #status predicted
F;459/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1, 'LSRG', 4-595 < SHE>
A; Residues: 1, 'LSRG', 4-595 < SHE>
A; Cross-references: EMBL: XG2055; NID: 935781; PIDN: CAA43982.1; PID: 935782
R; Shen, S.H.; Bastien, L.; Posner, B.I.; Chretien, P.
Nature 352, 736-739, 1991
A; Title: A protein-tyrosine phosphatase with sequence similarity to the SH2 domain of A; Reference number: S17234; MUID: 91343005; PMID: 1652101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGAVLAG---EFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSVYQLQYMSWPDRGVPSSPDHMLAMVEBARRLQGSGPE--PLCVHCSAGCGRTGVLCTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QEEGH-----SDYINGNFIRGV-----DGSLAYIATQGPLPHTLLDFWRLVWEFGVKVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             290 -- QGRDSNIPGSDYINANYIKNQLLGPDENAKTYIASQGCLEATVNDFWQMAWQENSRVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 LMACREIENGRKRCERYWAQEQEPLOTGLFCITLIKEKWINEDIMLRTLKVTFQKES---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REIWHYQYLSWPDHGVPSEPGGVLSFLDQINQRQESLPHAGPIIVHCSAGIGRTGTIIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DYVROLLLTQMI PPDFSLFDVVLKWRKQRPAAVQTEEQYRFLYHTVAQMFCST----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 WHITREVEKGRNKCVPYWPEVGMQRAYGPYSVINCGEHDITE-YKLRILQVSPLDNGDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.1%; Score 463; DB 1; Length 595; 32.9%; Pred. No. 3.6e-26; Live 56; Mismatches 110; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1,'LGRG',4-589,'VPSRGSERCCPQVAMPQP' <SH2>
A;Experimental source: breast carcinoma cells
A;Note: sequence revised in reference S20805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GDB:131389; OMIM:176883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 32.9%
hes 112; Conservative
A;Accession: A38189
                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: S17234
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protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN11, nonreceptor type 11 [validated] - hums N;Alternate names: BPTP-3; protein-tyrosine-phosphatase SHP-2; PTP1D; PTP2C; SH-PTP2; SH-C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: U. Mar-1994 #sequence revision 19-May-1994 #text_change 21-Jun-2002
C;Accession: J00805; A46210; A47244; S27398; C44929; S31767
R;Bastien, L.; Ramachandran, C.; Liu, S.; Adam, M. Biochem. Biophys: Res. Commun. 196, 124-133, 1993
A;Title: Cloning, expression and mutational analysis of SH-PTP2, human protein-tyrosine FA:Accession: J00805
A;Title: Identification, cloning, and expression of a cytosolic megakaryocyte protein-tyr A;Reference number: A41105; MUID:91288564; PMID:1648233 A;Accession: A41105
                                                                                                                                                                                                                                                                                                                                                                                                                                                      pe 3; GLGF domain homology; pr
tyrosine-specific phosphatase
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A;Residues: 1-593 ABAS.
A;Cross-references: GB:L07527; NID:g292406; PIDN:AAA17022.1; PID:g292407
A;Cross-references: GB:L07527; NID:g292406; PIDN:AAA17022.1; PID:g292407
R;Vogel, W.; Lammers, R.; Huang, J.; Ullrich, A.
Science 299, 1611-1614, 1993
A;Title: Activation of a phosphotyrosine phosphatase by tyrosine phosphorylation.
A;Reference number: A46210; MUID:93206095; PMID:7681217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OYIAWPDHGVPDDSSDFLDFVCHVRNKRAGKEEPVVVHCSAGIGRTGVLITME--TAMCL 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLQEEGHSDYINGNFIRGVDGSLA----YIATQGPLPHTLLDFWRLVWEFGVKVILMACR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 ARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-926 <GUA>
A;Cross-references: GB:M68941; NID:g190747; PIDN:AAA36530.1; PID:g190748
A;Experimental source: megakaryocytes, cell line MEG-10
C;Genetics:
                                                                                                                                                                                                                                                                                                                            A Gene: GDB:PTPN4
A; Cross-references: GDB:131387; OMIM:176878
A; Cross-references: GDB:131387; OMIM:176878
A; Cross-references: GDB:131387; OMIM:176878
A; Map position: 9431-9431
C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF dc C; Keywords: phosphortochein; phosphortochein; phosphortochein; protein; phosphortochein; protein; phosphortochein; protein; predicted; p; 852/Active site: Cys (phosphorystein; intermediate; #status predicted; p; 858/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.1%; Score 462; DB 1; Length 926;
.larity 37.6%; Pred. No. 7.5e-26;
Conservative 47; Mismatches 107; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 106; Conserv
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A;Cross-references: EMBL:X70766; NID:g35783; PIDN:CAA50045.1; PID:g35784
A;Experimental source: SK-BR-3 mammary carcinoma cells
A;Note: sequence extracted from NCBI backbone (NCBIP:127775)
A;Ahmad, S.; Banville, D.; Zhao, Z.; Fischer, E.H.; Shen, S.H.
Proc. Natl. Acad. Sci. U.S.A. 90, 2197-2201, 1993
A;Title: A widely expressed human protein-tyrosine phosphatase containing src homology

A; Residues: 1-593 < VOG>

protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN4, nonreceptor type 4 [validated] - human Nalternate names: PTPASE MEG
C)Alternate names: PTPASE MEG
C)Alternate names: PTPASE MEG
C)Aptes: 30-Mar-1992 #sequence\_revision 02-May-1994 #text\_change 21-Jun-2002
C)Accession: A41105
R)Gu, M.; York, J.D.; Warshawsky, I.; Majerus, P.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 5867-5871, 1991

us-10-087-993a-36.rpr

DD 500 QRSGMVQTEAQXRFIYMAV-QHYIETLQRRIEEEQKSKRKGHEYTNIKYSLA 550 RRSHILT 12	hosphatas	, A. sequence	A;Cross-references: GB:U38620; NID:g1054939; PIDN:AAC60049:1; PID:g1054940 C;Comment: This enzyme plays positive roles in mitogenic signaling and early development. C;Superfamily: protein-tyrosine-phosphates, nonreceptor type 6; protein-tyrosine-phosphates C;Keywords: phosphoriotein, phospharic monoseter hydrolase; tyrosine-specific phosphatase F;6-105,112-193/Domain: SH2 #status predicted <sh2> F;6-105,112-193/Domain: SH2 #status predicted <sh2> F;6-100/Domain: SH2 homology <sh3a> F;6-100/Domain: SH2 homology <sh3a></sh3a></sh3a></sh2></sh2>	F;273-510/Domain: protein tyrosine-phosphatase homology <ptp> F;559-570/Region: proline-rich F;459/Active site: Cys (phosphocysteine intermediate) #status predicted F;459/Active site: substrate phosphate (Arg) #status predicted F;542,547,580/Binding site: phosphate (Tyr) (covalent) #status predicted</ptp>	Query Match 18.7%; Score 45:  Best Local Similarity 33.9%; Pred. No cell Matches 118; Conservative 53; Misma	Qy 1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCS 47 :   :	ne-phosph  Qy 48 TVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRG 94  phosphatas Qy	OY 95 VDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWAQEQEPLQT 154	- F1 6	212 440	OY 270 Db 500		protein-tyrosine-phosphatase (BC 3.1.3.48), nonreceptor type 11 - mouse N;Alternate names: SH-PTP2; SH2-containing phosphotyrosine phosphatase Syp C;Species: Mus muscrilus (house mouse)	C,Daces: 22-281-1979 #Sequence_revision to NOV-1973 #Conc_commisc C,Accession: A46209 R,Feng, G.S.; Hui, C.C.; Pawson, T. Science 259, 1607-1611, 1993	
A; Reference number: A47386; MUID:93211929; PMID:7681589 A; Accession: A47386 A; Molecule type: mRNA A: Desiding: 1,503 A: A: MA	A; Experimental Source: umbilical cord A; Note: sequence extracted from NCBI backbone (NCBIN:128129, NCBIP:128131) A;Note: sequence extracted from NCBI backbone (NCBIN:128129, NCBIP:128131) A;Freeman Jr., R.M.; Plutzky, J.; Neel, B.G. Broc. Natl. Acad. Sci. U.S.A. B9, 11239-11243, 1992 A;Title: Identification of a human src homology 2-containing protein-tyrosine-pa;Recession: A47244; MUID:93087502; PMID:1280823 A;Accession: A47244 A;Molecule type: MRNA	A; Residues: 1.593 cFRE> A; Cross-Ireferences: GB:L03535; NID:g338081; PIDN:AAA36611.1; PID:g338082 A; Cross-Ireferences: GB:L03535; NID:g338081; PIDN:AAA36611.1; PID:g338082 A; Note: sequence extracted from NCBI backbone (NCBIN:119760, NCBIP:119761) R; Adachi, M.; Sekiya, M.; Miyachi, T.; Matsuno, K.; Hinoda, Y.; Imai, K.; Yachi, FRBS Lett. 314, 335-339, 1992 A; Title: Molecular cloning of a novel protein-tyrosine phosphatase SH-FTP3 with A: Paferance number. S27348; MITD:9416779; PMID:1281790	A; Accession: S27398 A; Molecule type: mRNA A; Residues: 1-534, W. 1, 535-547, P',549-593 < AD2> A; Residues: 1-534, W. 1, 535-547, P',549-593 < AD2> A; Cross-references: DDBJ: 1313540; NID: 9220071; PIDN: BAA02740.2; PID: 94519425 R; Adachi, M.; Sekiya, M.; Arimura, Y.; Takekawa, M.; Itoh, F.; Hinoda, Y.; Imai Cancer: Res 52, 737-740, 1992	D:1370651 DN:AAB21148.1; P	A:Experimental source: pre-B cell NALM-6 A;Note: sequence extracted from NCBI backbone (NCBIN:78088, NCBIP:78089) A;Note: the authors did not report the entire codon for residue 92 A;Comment: This ubiquitous enzyme plays a critical role in regulating physiological	C.Genetics: A;Gene: GDB:PTPN11 A;Cross-references: GDB:137093; OMIM:176876 A;Nap position: 12q24.1-12q24.1	C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phospi C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas F;6-100/Domain: SH2 homology <sh2a> F;112-214/Pomain: SH2 homology <sh2b></sh2b></sh2a>	F;273-510/Domain: protein-tyrosine-phosphatase homology <ptp> F;459/Active site: Cys (phosphocysteine intermediate) #status predicted F;465/Binding site: substrate phosphate (Arg) #status predicted</ptp>	Query Match 18.7%; Score 453; DB 1; Length 593; Best Local Similarity 33.8%; Pred. No. 2e-25; Matches 119; Conservative 53; Mismatches 126; Indels 54; Gaps 12	OY 1 MSRSIDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCS 47	QY 48 TVAGSRPENVRKNRYKDVLPYDQTRVILSLLQSEGHSDYINGNFIRG 94  DD 265 RKEGQRQENKNRNRYKNILDFDHTRVVLHDGDPNEPVSDYINANIIMPEFETKCNN 320	Qy 95 VDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWAQEQEPLQT 154	QY 155 GLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVESSPDHMLAMV 21.1	QY 212 EEARRLQGSGPBPLCVHCSAGCGRTGVLCTVDYVRQLLLIQMIPPDFSLFDVVLKMRK 269	

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P,463/Active site: Cys (phosphocysteine intermediate) #status predicted P,469/Binding site: substrate phosphate (Arg) #status predicted
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Best Local Similarity 32.4%;
Matches 125; Conservative 51
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A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-585 <FEN>
A;Residues: 1-585 <FEN>
A;Residues: cxtracted from NCBI backbone (NCBIP:127770)
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosph C;Reywords: phosphorotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase F:110-214/Nomain: CHI chosphatase 
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A53593; S29281
C;Accession: A53593; S29281
T;Mei, L., Doherty, C.A., Huganir, R.L.
J. Biol. Chem. 269, 12254-12262, 1994
A;Title: RNA splicing regulates the activity of a SH2 domain-containing protein tyrosine
A;Reference number: A53593; MUID:94216346; PMID:7512964
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A;Residues: 24-31;36-54;56-89;100-103,'X',105-108;'X',113-120;132-155;179-198;214-233;24
C;Superfamily: protein-tyrosine-phosphatase, nonecceptor type 6; protein-tyrosine-phosph
C;Keywors alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrosi
F;6-100/Domain: SH2 homology <SH2A>
F;112-214/Domain: SH2 homology <SH2B>
F;273-514/Domain: protein-tyrosine-phosphatase homology <PTP>
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A,Status: preliminary
A,Rolecaule type: mRNA
A,Rolecaule type: mRNA
A,Rolecaule type: mRNA
A,Rolecaule type: mRNA
A,Rolecaule type: mRNA
A,Rolecaule type: mRNA
A,Cross-references: GB:U05963; NID:g458332; PIDN:AAA19133.1; PID:g458333
B,Cross-references: GB:U05963; NID:g458332; PIDN:AAA19133.1; PID:g458333
B,Cross-references: GB:U05963; NID:g458332; PIDN:AAA19133.1; PID:g458333
B,Cross-reference non and characterization of a rat liver protein-tyrosine phosphatase
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F;2773-514/Domain: protein-tyrosine-phosphatase homology <PTP>
F;273-214/Domain: protein-tyrosine-phosphatase homology <PTP>
F;463/Active site: Cys (phosphocysteine intermediate) #status predicted
F;469/Binding site: substrate phosphate (Arg) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.6%; Score 451; DB 2; Length 58 31.0%; Pred. No. 2.7e-25; ive 59; Mismatches 142; Indels
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C,Accession: A44267
R;Howard, P.K.; Sefton, B.M.; Firtel, R.A.
R;Howard, P.K.; Sefton, B.M.; Firtel, R.A.
A;Howard, P.K.; Sefton, B.M.; Firtel, R.A.
A;Hitle: A37-647, 1992
A;Hitle: Analysis of a spatially regulated phosphotyrosine phosphatase identifies tyrosin A;Reference number: A44267, MUID:93046662; PMID:1423620
A;Accession: A44267
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C;Superfamily: Dictyostelium protein-tyrosine-phosphatase, nonreceptor type 1; protein-ty
C;Keywords: phosphogrotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F;121-459/Domain: protein-tyrosine-phosphatase homology #status atypical <PTP>
F;310/Active site: Cys (phosphocysteine intermediate) #status predicted
F;316/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 1 - slime mold (Dictyosteliv
                                                                                                                  14;
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C;Date: 30-Apr-1993 #sequence_revision 08-Mar-1996 #text_change 24-Apr-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 EVFGTYSVELVEVIQDP--ERELITRNIRLTFEGETRDITQYQYEGWPDHNI---PDHTQ
                                                                                                                                                                                                                         1 MSRSIDSARSFLERLEARGGREGAVLA-----GEFSDI--QACSAAWKADGVCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 TVAGSRPENVRKONRYKDVLPYDQTRVILSLLQEEGH-----SDYINGNFI-----RG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLFCITLIKEKWINEDIMLRTLKVTFQKES-----RSVYQLQYMSWPDRGVPSSPDHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 LAMVEBARRLOGS - - GPEPLCVHCSAGCGRIGVLCTVDYVRQLLLTQMIPPDFSLFDVVL
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                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                 62;
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thes 88; Indels 1
                                                                                                            58; Mismatches 141; Indels
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53; Mismatches
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Score 449;
Pred. No. 3
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Search completed: August 17, 2004, 20:44:35 Job time : 18 secs

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# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

August 17, 2004, 20:29:38; Search time 14 Seconds (without alignments) 1703.438 Million cell updates/sec Run on:

US-10-087-993A-36 2424 1 MSRSLDSARSFLERLEARGG......NLRIGRPKGPRDPPAEWTRV 458

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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P10586 homo sapien 22468 homo sapien 29bmn8 caenorhabdi 299m80 mus musculu 014522 homo sapien P28928 mus musculu P49445 rattus norv 013332 homo sapien P23471 homo sapien P23471 homo sapien P23471 rattus norv
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# ALIGNMENTS

RESULT 1

KW Hydrolase.
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                             PROTEIN-TYROSINE PHOSPHATASE.
PHOSPHOCYSTEINE INTERMEDIATE (BY
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                     OF1E45339BD4613E CRC64;
                                                                                                                                                                 PDB; 1JEG; 31-OCT-01.
MGD; MGI:107170; PtpnB.
InterPro; IPR0000342; TYR_phosphatase.
InterPro; IPR0000342; TYR_phosphatase.
Pfam; PF00102; Y_phosphatase; 1.
PRINTS; PR00700; PRTPPHPHTASE.
SMART; SM00194; PTPC; 1.
PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE 2; 1.
Hydrolase; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                     802 AA; 89714 MW;
                                                                                                                               EMBL; M90388; AAA39994.1; -. PIR; B44390; B44390.
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Matches 161; Conservative
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                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                   61 RYKDVLPYDQTRVILSILQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120
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                                                                                                                                                                                                                                                                                                                                                                                                 181 QKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEBARRLQGSGPEPLCVHCSAGCGRTGVLC
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                                                                                                                                                                                                                                                                                                                                                   121 BFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           threonine-rich sequences.";
Mol. Cell. Biol. 12:2396-2405(1992).
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein tyrosine + phosphate + H(2)0 = protein tyrosine + phosphate.
-!- SUBCELIULAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: Spleen, thymus, lympH node and bone marrow.
-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matthews R.J., Bowne D.B., Flores E., Thomas M.L.;
Characterization of hematopoietic intracellular protein tyrosine
phosphatases: description of a phosphatase containing an SH2 domain
and another enriched in proline, glutamic acid, serine, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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10-0CT-2003 (Rel. 42, Last annotation update)
Protein-tyrosine phosphatase, non-receptor type 8 (EC 3.1.3.48)
(Hematopoietic cell protein-tyrosine phosphatase 70Z-PEP).
                     (BY
                                                                                             Length 458;
                   PHOSPHOCYSTEINE INTERMEDIATE
                                                                                                                                   Indels
                                                     46BCA1E17C2C78B1 CRC64;
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                                                                                             Score 2424; DB 1;
Pred. No. 1.7e-160;
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                                                                                                         100.0%; Pred. ....
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                                       SIMILARITY
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MEDLINE=92236615; PubMed=1373816;
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                                                         458 AA; 50384 MW;
                                                                                             100.08;
                                                                                                                                 Conservative
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                                                                                                                 Similarity
                     229
                                                                                                                                   458;
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                   ACT_SITE
                                                       SEQUENCE
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                                                                                             Query Match
                                                                                                                   Local
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PING MOUSE

RESULT

7 146 144 203 265 325 308 326 LLAIPRPPGGVLRSISVPGS-----PGHAMAD--TYAEEQKRGAPAGAGSGTQTGTGTG 377 :|| :| :| :| | :| | :| | :| | 362 86 84 :|| |||: |||:||| :| | ::| 264 EMRTQRPSLVQTQEQYELVYSAVLELF-----KRHMDVISDNHLG------REIQA 25 ASEFLKLKRQSTKYKADKIYPTVAQRPKNIKKNRYKDILPYDHSLVELSLLTSDEDSSY 87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA 147 QEQE-PLOTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD 206 HMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLIQMIPPDFSLFDVVL 266 KWRKORPAAVOTEEOYRFLYHTVAQMFCSTLQNASPHYQNIKENCAPLYDDALFLRTPQA AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY 31; Gaps Protein-tyrosine phosphatase, non-receptor type 22 (EC 3.1.3.48) (Hematopoietic cell protein-tyrosine phosphatase 702-PEP) (Lymphoid phosphatase) (LyP). Eukaryota; Marazona; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI\_TaxID=9606; Length 802; Indels 31.2%; Score 755.5; DB 1; 44.0%; Pred. No. 8.2e-45; tive 55; Mismatches 119; PTNM HUMAN STANDARD; PRT; 807 AA. Q9Y2R2; 095063; 095064; 28-FEB-2003 (Rel. 41, created) 10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)

us-10-087-993a-36.rsp

86

AGEFSD1QACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRV1LSLLQEEGHSDY

27

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                                                              SIMILARIIY).
ELADDRSSPPPPLFBRTLESFFLADEDCMQAQSIETYSTSY
PDTWENSTSSKQTLKTPGKSFTRSKSLKILRNWKKSICNSC
PPNKPAESVQSNNSSSFLNFGFANRFSKFKGPRPPPTWNI
SEQUENCE FROM N.A. (ISOPORMS 1 AND 2), AND CHARACTERIZATION.
MEDLINE=99168989; PubMed=10068674;
Cohen S., Dadi H., Shaoul E., Sharfe N., Roifman C.M.;
"Cloning and characterization of a lymphoid-specific, inducible human protein tyrosine phosphatase, Lyp.";
Blood 93:2013-2024(1999).
                                                                                                                                                                                                                                                                                                                                                                                          -> GKNFSML (in isoform 2).

/F71d=VSB 000134.

Y -> G (IN REF. 1).

V -> G (IN REF. 2).

G -> V (IN REF. 2).

I -> IV (IN REF. 2).

L -> P (IN REF. 2).

L -> P (IN REF. 2).

R -> W (IN REF. 2).

R -> W (IN REF. 2).

R -> W (IN REF. 2).

R -> W (IN REF. 2).

R -> W (IN REF. 2).

R -> W (IN REF. 2).

R -> W (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                               EMBL; AF001846; AAD00904.1; --
EMBL; AF071847; AAD00905.1; --
EMBL; AF077031; AAD27764.1; --
HSSP; P29350; 1GWZ.
Genew; HGNC:9652; PTPN22.
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1126
1247
620
620
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126
147
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1240
420
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742
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                                                      146
                                                                                                                                                                         203
              84
                                                                           85 INANFIKGVYGPKAYIATQGPLSTILLDFWRMIWEYSVLIIVWACMEYEMGKKKCERYWA
                                                                                                                                                        145 EPGEMQLEFGPFSVSCEAEK-RXSDYIRTLKVKFNSETRTIYQFHYKNWFDHDVPSSID
                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-93203262; PubMed=8454633;
Yang Q.C., Tonks N.K., Sommercorn J.;
Yang Q.C., Tonks N.K., Sommercorn J.;
"Cloning and expression of PTP-PEST. A novel, human, nontransmembrane protein tyrosine phosphatase.";
"Cloning and expression of PTP-PEST. A novel, human, nontransmembrane protein tyrosine phosphatase.";
"I siol. Chem. 268:6622-6628(1993).
"N AND VARIANT COLON CANCER ARG-61.
                                                        INGNFIRGVDGSLAYIATOGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA
                                                                                                                                                                                                                 HMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL
147 QEQE-PLOTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEBS Lett. 339:222-228(1994).
-!-CATALVITA: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate
-!-SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- DISEASE: DEFECTS IN PIPNIZ ARE FOUND IN SOME COLON CANCERS.
-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 268:6622-6628(1993).

[3]
SEQUENCE OF 59-136 FROM N.A., AND VARIANT COLON CANCER ARG-61.
SEQUENCE OF 59-136 FROM N.A., AND VARIANT COLON CANCER ARG-61.
Takekawa M., Itoh F., Hinoda Y., Adachi M., Ariyama T., Inazawa J.,
Imai K., Yachi A.;
"Chromosomal localization of the protein tyrosine phosphatase Gl ger and characterization of the aberrant transcripts in human colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human),
bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 (EC 3.1.3.48)
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TISSUE=COlon;

MEDLINE=3112015; PubMed=1472029;

Takekawa M., Itoh F., Hinoda Y., Arimura Y., Toyota M., Sekiya N.

Adachi M., Imai K., Yachi A.;

"Cloning and characterization of a human cDNA encoding a novel putative cytoplasmic protein-tyrosine-phosphatase.";

Biochem. Biophys. Res. Commun. 189:1223-1230(1992).
                                                                                                                                                                                                                                                                                            266 KWRKORPAAVQTEEQYRFLYHTVAQMF---CSTLQNASPHYQNIKENCAP 312
                                                                                                                                                                                                                                                                                                                   005209; Q16130;
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein-tyrosine phosphatase, non-receptor type
(Protein-tyrosine phosphatase G1) (PTPG1).
                                                                                                                                                                                                                                                                                                                                                                                                                                    780 AA
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Gaps

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DB 1; Length 807; Indels

Query Match
30.0%; Score 727.5; DB 1;
Best Local Similarity 46.9%; Pred. No. 7.1e-43;
Matches 136; Conservative 56; Mismatches 93;

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296
328
380
775 AA;
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NCBI_TaxID=10090;
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231
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Matches 194;
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                                                                                                                                                     MIM; 600075; ... Crytcplasm; TAS.

RGG; GG:0005573; Crytcplasm; TAS.

RGG; GG:0005625; Crscluble fraction; TAS.

RGG; GG:0006470; P:protein amino acid dephosphorylation; TAS.

RGG; GG:0006470; P:protein amino acid dephosphorylation; TAS.

InterPro; IPR000387; TYR_phosphatase.

InterPro; IPR000387; TYR_phosphatase.

RAST; ER00102; Yphosphatase; 1.

PRINTS; PR00102; Yphosphatase.

SMART; SM01094; PTPC; 1.

RRAST; SW0183; TYR_PHOSPHATASE.

RRAST; PR00185; TYR_PHOSPHATASE.

RROSTTE; PS50056; TYR_PHOSPHATASE_2; 1.

RROSTTE; PS50055; TYR_PHOSPHATASE_2; 1.

RAGGIASE; Disasase mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 VKVILMACREIENGRKRCERYW-AQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 DYVROLLLIOMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPH 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYK
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   344
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01-FBE-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein-tyrosine phosphatase, non-receptor type 12 (EC 3.1.3.48)
(Protein-tyrosine phosphatase P19) (P19-PTP) (MPTP-PEST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GAQKIADGVNEINTENMVSSIEPEKQDSPPKPPR--TRSCLVEG 347
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SINTLARITY).
K -> K (in colon cancer).
/FTIG=VAR 006385.
V -> I (IN REF 2).
V -> I (IN REF 2).
W, 48F7BEFPDAEF7512 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN-TYROSINE PHOSPHATASE.
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    or send an email to license@isb-sib.ch)
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                                   EMBL; D13380; BAA02648.1; -.
EMBL; M93425; AAA36529.1; -.
EMBL; S69184; AAB30047.2; -.
PIR; JC1368; JC1368.
HSSP; Q06124; 2SHP.
Genew; HGNC:9645; PTPN12.
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780 AA; 88092 MW;
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Best Local 8
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    OCCEPTATION
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"Murine protein tyrosine phosphatase-PEST, a stable cytosolic protein tyrosine prosphatase.";
tyrosine phosphatase.";
Blochem. J. 308:425-432(1995).
--- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYK
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ilarity 25.0%; Pred. No. 3.3e-41;
Conservative 84; Mismatches 162; Indels 336; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tyrosine + phosphare.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
                                                                                                                                                                                                                                                                                 REVISIONS TO 297-416.

MEDILINES 29112015, PubMed=1472029;
Takekama M., Itoh F., Hinoda Y., Arimura Y., Toyota M., Sekiya M., Adachi M., Imai K., Yachi A.;
Adachi M., Imai K., Yachi A.;
Cloning and characterization of a human cDNA encoding a novel putative cytoplasmic protein-tyrosine-phosphatase.";
Bjochem. Biophys. Res. Commun. 189:1223-1230(1992).
SEQUENCE FROM N.A.
MEDLINE=22272714; PubMed=1590786;
MEDLINE=22272714; PubMed=1590786;
Men Hertog J., Pals C.E., Jonk L.J., Kruijer W.;
"Differential expression of a novel murine non-receptor protein tyrosine phosphatase during differentiation of P19 embryonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY
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K -> N (IN REF. 1).

KQDEP -> DETS (IN REF. 1).

W -> V (IN REF. 1).

7106D73F5014E411 CRC64;
                                                                                                                                                                                      carcinoma cells.";
Biochem. Biophys. Res. Commun. 184:1241-1249(1992)
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EMBL, X86781; CAA60477.1; -.
PIR, S55344; S55345.
HSSP, Q06124; 281P.
MGD; MG1:104673; Ptpn12.
InterPro; IPR000387; TYR_PP.
InterPro; IPR00024; TYR_PP.
PEAM; PF00102; Y_phosphatase.
PRINTS; PR00109; PRTYPHPHTASE.
SMART; SW00194; PTP? 1.
PROSITE; PS00065; TYR_PHOSPHATASE 1; 1.
PROSITE; PS00065; TYR_PHOSPHATASE 2; 1.
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STRAIN-BALB/c;
MEDLINE=95289971; PubMed=7772023;
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         305 GAQKIRDGNEITTGTMVSSIDSEKQDSPPPKPPRTRSCLVEGDAKEEILQPPEPHPVPPI 364
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                                                                                                                                                                                         425 IDKKLERNLSFEIKKVPLQEGPKSFDGNTLLNRGHAIKİKSASSSVVD-----RİSKPQE 479
                                                                                                                                                                                                                             -----IPRP-----9GGVLRSI- 340
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                                              ESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPBPLCVHCSAGCGRTGVLCTV
                                                                        DYVROLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTBEQYRFLYHTVAQMFCSTLQ----
                                                                                                                                                                                                                                                                                                        ------GAPAGAGSGTQTGTGTGA----RSAEEAPLYSKVTPR-----
                                                                                                                                                                                                                                                                                                                                                                                  456
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15-JUL-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
(Receptor-type protein-tyrosine phosphatase V precursor (EC 3.1.3.48)
(Embryonic stem cell protein-tyrosine phosphatase) (ES cell
                                                                                                                                                                                                                                                                                                                                                                                 ------ADOSPAGSGAYEDVA-GGAQTGGLGFNLRIGRPKGPRDPPAEWT
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUB=Embryonic stem cells;
MEDLINES=97.09513; PubMed=8951793;
Lee K., Nichols J., Smith A., Smith A.,
"Identification of a developmentally regulated protein tyrosine
phosphatase in embryonic stem cells that is a marker of
pluripotential epiblast and early mesoderm.";
Mech. Dev. 59:153-164(1996).
                                                                                                                                                                                                                                                                                                                                             ---AQRPGAHAEDARGTLPGRVP---------
                                                                                                                                                   -----NASP------
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Mech. Dev. 61:213-215(1996).
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FUNCTION: May play a role in the maintenance of pluripotency. Down-regulated during differentiation. CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                         tyrosine + phosphate.
--- SUBCELLULAR LOCATION: Type I membrane protein.
--- DEVELOPMENTAL STAGE: Detectable in the epiblast of oocytes and throughout early mouse embryo development. In adult, expression localized in gonadal germ calls.
--- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
--- SIMILARITY: Contains 10 fibronectin type III domains.
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FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
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FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 7.
FIBRONECTIN TYPE-III 9.
FIBRONECTIN TYPE-III 9.
FIBRONECTIN TYPE-III 9.
FIBRONECTIN TYPE-III 10.
PROTEIN-TYROSINE PHOSPHATASE 1.
PROTEIN-TYROSINE PHOSPHATASE 2.
PHOSPHOCYSTEINE INTERNEDIATE (BY
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INTERPO: JPR0000(1) PR000(1) FIN III.
INTERPO: JPR000(1) FIN III.
INTERPO: JPR000(1) FIN III.
INTERPO: JPR000(1) FIN III.
INTERPO: JPR000(1) TYR PHOSPHATASE.
INTERPO(10) PROUD(1) Y_Phosphatase; J.
PR001(1) PR001(1) PR1YPHPHTASE.
SMART; SM001(1) PR001(1)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC.
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HSSP; P18052; 1YFO.
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                                                                                                                                                                                  1245
                                                                                                                                                                                                                                                                                   1132 SHSFRQSYEAKSARAHQAFFQEFEELKEVGKDQ-----PRLEAEHPANITKNRYPHVLP 1195
                                                                                                                                                                                                                                         1246 IMLTVGMENGRVLCEHYWPVNSTPVTHGHITTHLLAEESEDEWTRREFQLQH---GAEQK 1302
                                                                                                                                                     127
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                                                                                                                                                                                                                                                                                                                           LCTVDYVRQLLLIQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQN 298
                                                                                                                                                                                                                                                                                                                                                                                 299 ASPH----YQNIXENCA--PLYDDALFLRTPQAL-LAIPRPPGGVLRSISVPGSPGHAMA 351
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-!- FUNCTION: Plays a key role in hematopoiesis. This PTPase activity may directly link growth factor receptors and other signaling proteins through protein-tyrosine phosphorylation. The SHZ regions may interact with other cellular components to modulate its own phosphatase activity against interacting substrates (By
                                                                                                                                                       YDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVI
                                                                                               8 ARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLP
                                                                                                                                                                            1186 YDHSRVRLTQLSGEPHSDYINANFIPGYSHPQEIIATQGPLKKTVEDFWRLVWEQQVHVI
                                                                                                                                                                                                                                                                    184 SRSVYQLQYMSWPDRGVPSSPDHMLAMV----EEARRLQGSGPEPLCVHCSAGCGRTGV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                      Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tyrosine + phosphate.
--- SUBINIT: Monomer (By similarity). Binds PTPNS1 (By similarity).
--- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
--- SIMILARITY: Contains 2 SH2 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The rat SH2-containing protein-tyrosine phosphatase SHP-1 is a positive regulator of NGF-induced neuronal differentiation of PC12 cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amoutation update)
Protein-tyrosine phosphatase, non-receptor type 6 (EC 3.1.3.48)
(Protein-tyrosine phosphatase SHP-1)
 (POTENTIAL)
                                                                      52;
                                        20.0%; Score 485; DB 1; Length 1705; larity 33.4%; Pred. No. 1e-25; Conservative 52; Mismatches 163; Indels 5:
982 982 N-LINKED (GLCNAC. . .) (POT. 1705 AA; 186795 MW; 2783755F15387D5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCHHSQEQLALVEESPADNMLAASLFPGGPSGRDHVVLTGS 1514
                                                                                                                                                                                                                                                                                                                                                                                                                                         352 DIYAEEQK------RGAPAGAGSGIQIGT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat)
                                                     Local Similarity
hes 134; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=10116;
  CARBOHYD
SEQUENCE
                                            Query Match
                                                             Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 LMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKES--- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGAVLAG---EFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          350 WMTTREVEKGRNKCVPYWPEVGTQRVYGLYSVTNCKEHDTAE-YKLRTLQISPLDNGDLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 RSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPB--PLCVHCSAGCGRTGVLCTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29; Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTT, 595 AA.
P29351; 035128; Q63872; Q63873; Q63874; Q921G3; Q9QVA6; Q9QVA7; Q9QVA5; Q90VA6; Q9QVA7; Q9QVA6; Q9QVA7; Q9QVA6; Q9RC-1992 (Rel. 24, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Protein-tyrosine phosphatase, unon-receptor type 6 (EC 3.1.3.48)
Protein-tyrosine phosphatase, 1C) (PTP-1C) (Hematopoietic cell protein-tyrosine phosphatase)
(702-SHP) (SH-PTP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYVROLLLTQMIPPDFSLFDVVLKWRKQRPAAVQTBEQYRFLYHTVAQMFCST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN-TYROSINE PHOSPHATASE.
PHOSPHOCYSTEINE INTERMEDIATE
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
19.9%; Score 482.5; DB 1; Length
Best Local Similarity 36.9%; Pred. No. 4.5e-26;
Matches 108; Conservative 52; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29364B22E8F45C87 CRC64;
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PROSITE; PS00183; TYR PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR PHOSPHATASE 2; 1.
PROSITE; PS50055; TYR PHOSPHATASE PTP; 1.
Hydrolase; SH2 domain; Repeat.
                                                                                                                                                                                                                            InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000342; TYR_PP.
Pfan; PF001027; Y phosphatase; 1.
Pfan; PF001027; Y phosphatase; 1.
PRINTS; PR00100; PRTYPHPHTASE.
PRINTS; PR00401; SH2DOMAIN.
SWART; SM00194; PTPC; 1.
SWART; SM00194; PTPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SH2 1.
SH2 2.
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PTPN6 OR PTP1C OR HCP OR HCPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                613 AA; 69578 MW;
                                                                                                                                                                              EMBL; U77038; AAD00262.1; -.
HSSP; P29350; 1GWZ.
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215
517
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Biol. Chem. 267:23447-23450(1992)

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MEDLINE=2238825'; PubMed=12477932;

MEDLINE=2238825'; PubMed=12477932;

MISTAINE=2238825'; PubMed=12477932;

MISTAINE=2238825'; PubMed=12477932;

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

M. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Diatchenko L., Marusina K., Frrmer A.A., Rubin G.M., Hong L.,

Rapleron M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rotherth A., Schein J.E., Jones S.J.M., Marra M.A.,

Generation and initial analysis of more than 15,000 full-length
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Yenng Y.-G., Berg K.L., PixLey F.J., Angeletti R.H., Stanley E.R.;
Protein tyrosine phosphatase-IC is rapidly phosphorylated in tyrosine
"Protein response to colony stimulating factor-1.";
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND VARIANTS MOTHEATEN AND VIABLE MOTHEATEN.
STRAIN=CS7BL/61; TISSUB=Bone marrow;
MEDLINE=9313972; PubMed=8324828;
Schultz L.D., Schweitzer P.A., Rajan T.V., Yi T., Ihle J.N.,
Matthews R.J., Thomas M.L., Beier D.R.;
"Mutations at the murine motheaten locus are within the hematopoietic cell protein-tyrosine phosphatase (Hcph) gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SUBUNIT.
STRAIN=C3H; TISSUB=Adrenal gland;
MEDLINE=99481302; PubMed=10419485;
MARTÍNE=9948302; PubMed=10419485;
MARTÍN A., Tsui H.W. Shulman M.J., Isenman D., Tsui F.W.;
"Murine SHP-1 splice variants with altered Src homology 2 (SH2)
domains. Implications for the SH2-mediated intramolecular regulation
                                                                                                                                                                                                                    Matthews R.J., Bowne D.B., Flores E., Thomas M.L.; And a control of hematopoietic intracellular protein tyrosine phosphatases: description of a phosphatase containing an SH2 domain and another enriched in proline, glutamic acid, serine, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 54-68; 128-135; 137-151; 242-252; 278-285; 293-308 AND 373-382, AND PHOSPHORYLATION.
                                   Yi T., Cleveland J.L., Thie J.N.;

"Protein tyrosine phosphatase containing SH2 domains:
characterization, preferential expression in hematopoietic cells,
localization to human chromosome 12p12-p13.";

Mol. Cell. Biol. 12:836-846(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ansari-Lari M.A., Oeltjen J.C., Schwartz S., Zhang Z., Muzny D.M.
Lu J., Gorrell J.H., Chinault A.C., Belmont J.W., Miller W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Comparative sequence analysis of a gene-rich cluster at human chromosome 12p13 and its syntenic region in mouse chromosome 6. Genome Res. 8:29-40(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
MEDLINE=98112780; PubMed=9445485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 274:21725-21734(1999).
                                                                                                                                                                                                                                                                                                                              Mol. Cell. Biol. 12:2396-2405(1992).
                                                                                                                                                                                               MEDLINE=92236615; PubMed=1373816;
STRAIN=DBA/2;
MEDLINE=92123209; PubMed=1732748;
                                                                                                                                                                                                                                                                                                              sednences.
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                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                threonine-rich
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MEDINE=98380500; PubMed=9712903;

MEDLINE=98380500; PubMed=9712903;

Medilette A., Thibaudeau E., Latour S.;

Veillette A., Thibaudeau E., Latour S.;

Veillette A., Thibaudeau E., Latour S.;

With protein tyrosine phosphatase SHP-1 in macrophages.";

J. Biol. Chem. 273:22719-22728(1998).

I. FUNCTION: Plays a key role in hematopoiesis. This PTPase activity at directly link growth factor receptors and other signaling proteins through protein-tyrosine phosphorylation. The SH2 regions may directly link growth factor receptors and other signaling proteins through protein-tyrosine phosphorylation. The SH2 regions may interact with other cellular components to modulate its own phosphatase activity against interacting substrates.

C. -- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.

C. -- SUBGELIULAR LOCATION: Cytoplasmic.

--- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                   protein-tyrosine phosphatase family
                                                                                                                                                                                                                                                                                                                                                                       Isold=P29351-3; Sequence=VSP_005132, VSP_005133; TISSUE SPECIFICITY: Expressed predominantly in hematopoietic
                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PTM: Phosphorylated on tyrosine residues.
-!- SMILARITY: Belongs to the protein-tyrosi
Non-receptor class subfamily.
-!- SIMILARITY: Contains 2 SH2 domains.
                                                                                                                                                                                                                                                                                                                                          sold=P29351-2; Sequence=VSP_005131;
                                                                                                                                                                                                                                                                                                            IsoId=P29351-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
PROSITE; PS50001; SH2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000980; SH2.
InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000342; TYP_PP.
Ffam; PF00107; SH2; 2.
Pfam; PF00107; Y phosphatase; 1.
PRINTS; PR001001; SH2DOMAIN.
PRINTS; PR00401; SH2DOMAIN.
SNART; SM00194; PTPC; 1.
SNART; SM00194; PTPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:96055; Hcph.
                                                                                                                                                                                                                                                                                                Name=1;
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CARBOHYD
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     ω,
                                                                                                                                       | SIMILARITY |
| MUR. -> MLSRG (in isoform 2). |
| /FTId=VSP_005131. |
| Missing (in isoform 3). |
| /FTId=VSP_005132. |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :| | | : | | | : | | | 348 WATTREVEKGRNKCVPYWPEVGTQRVYGLYSVINSREHDIAE-YKLRILQISPLDNGDLV 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 RSVYQLQYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPE--PLCVHCSAGCGRTGVLCTV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGAVLAG---EFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mauro L.J., Olmsted B.A., Skrobacz B.M., Mourey R.J., Davis A.R., Dixon J.E.,
Dixon J.E.,
"Identification of a hormonally regulated protein tyrosine
phosphatase associated with bone and testicular differentiation.";
J. Biol. Chem. 269:30659-30667(1994).
-!- FUNCTION: May function in signaling pathways during bone
remodeling, as well as serve a broader role in cell inceractions
associated with differentiation in bone and testis. Optimal pH for
phosphatase activity is 5.6. Associated with differentiation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 LMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKES---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REIMHYQYLSWPDHGVPSEPGGVLSFLDQINQRQESLPHAGPIIVHCSAGIGRIGTIVI
  Phosphorylation; Alternative splicing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annocation update)
16-MAR-2004 (Rel. 43, Last annocation update)
16-MAR-2004 (Rel. 43, Last annocation update)
17-MAR-2004 (Rel. 43, Last annocation phosphatase (EC 3.1.3.48)
18-MAR-2001 (EMbryonic stem cell protein-tyrosine phosphatase) (ES cell phosphatase) (Osteotesticular protein-tyrosine phosphatase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYVROLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCST 295
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                                                                             PROTEIN-TYROSINE PHOSPHATASE.
PHOSPHOCYSTEINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.6%; Score 475.5; DB 1; Length 595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Pred. No. 1.3e-25; 53; Mismatches 105;
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MEDLINE=95074080; PubMed=7527035;
  Repeat;
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Matches 106; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                Isolaeq64612-2; Sequence=Not described;
Note=No experimental confirmation available;
Note=No experimental confirmation available;
TISSUE SPECIFICITY: Bone and testis. In the latter, restricted to
the basal portion of the seminiferous tubule.
BEVELOPMENTAL STAGE: Up-regulated in differentiating cultures of
primary osteoblasts and down-regulated in late stage mineralizing
cultures. In testis, expression is highest between stages; and
vII when maturing spermatids remain buried within the sertoli
bone and testis.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein tyrosine + phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                     Event=Alternative splicing, Named isoforms=2;
Comment=A presumed alternate transcript of 4.8-5.0 kilobases,
which may lack PTP domains, is present in proliferating
osteoblasts, but not detectable at other stages;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epithelium.
-!- INDUCTION: By parathyroid hormone and CAMP analogs.
-!- PTM: The cytoplasmic domain contains potential phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sites.
-!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
-!- SIMILARITY: Contains 10 fibronectin type III domains.
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FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 5.
FIBRONECTIN TYPE-III 7.
FIBRONECTIN TYPE-III 9.
FIBRONECTIN TYPE-III 9.
FIBRONECTIN TYPE-III 9.
FUBRONECTIN TYPE-III 9.
FUBRONECTIN TYPE-III 9.
FUBRONECTIN TYPE-III 10.
PROTEIN-TYROSINE PHOSPHATASE 1.
PROTEIN-TYROSINE PHOSPHATASE 2.
PHOSPHOCYSTBINE INTERMEDIATE (BY
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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R InterPro; IPR003961; FN_III.

R InterPro; IPR000242; TYR_phosphatase.

R Pfan; PP00041; fin3, 7.

R Pfan; PP00041; fin3, 7.

R Pfan; PR00102; Y_phosphatase; 1.

R Pfan; PR00102; Y_phosphatase; 1.

R RFANTS; PR00104; FNTS; 1.

R RFANTS; PR00106; FNTS; 1.

R RFANTS; PR00106; FNTS; 1.

R RRAT; SM00194; PTPC; 1.

R RRAT; SM00194; PTPC; 1.

R ROSITE; PS00055; TYR_PHOSPHATASE_1; 1.

R ROSITE; PS00055; TYR_PHOSPHATASE_2; 1.

R RATIONARE; TRANSMEMBIRATE; 2, 1.

R Alternative splicing.

R Alternative splicing.

R SIGNAL
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                      Name=1;
IsoId=Q64612-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L36884; AAA63911.1; -.
HSSP; P18052; 1YFO.
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Nature 352:736-739(1991)
   1188 HSRVRLTQLPGEPHSDYINANFIPGYSHTQEIIATQGPLKKTLEDFWRLVWEQQVHVIIM 1247
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ID PTING HUMAN

STANDARD; PRT; 595 AA.

DT P21350, 9096948;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 10-CCT-2003 (Rel. 42, Last annotation update)

DF 10-CCT-2003 (Rel. 42, Last annotation update)

DF Protein-tyrosine phosphatase it? (PTP-1C) (Hematopoietic cell

DE protein-tyrosine phosphatase (SH-PIP1) (Protein-tyrosine phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yi T., Cleveland J.L., Ihle J.N.;
"Protein tyrosine phosphatase containing SH2 domains:
characterization, preferential expression in hematopoietic cells, and
localization to human chromosome 12p12-p13.";
Mol. Cell. Biol. 12:836-846(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 SVYOLQYMSWPDRGVPSSPDHMLAMV----EEARRLQGSGPEPLCVHCSAGCGRTGVLCT
                                                                                                                                                                                                                                                                                                                                                    SFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB=Breast;
MEDLINE=91343005; PubMed=1652101;
MEDLINE=91343005; PubMed=1652101;
Shen S.H., Bastien L., Posner B.I., Chretien P.;
"A protein-tyrosine phosphatase with sequence similarity to the domain of the protein-tyrosine kinases.";
               (POTENTIAL)
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MEDLINE=92123209; PubMed=1732748;
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1711 AA;
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     CARBOHYD
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Nature 353:868-868(1991)
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   B42031; S20825.
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                                                                                                                                                             tyrosine + phosphate.
SUBUNIT: Monomer (By similarity). Binds PTPNS1, LILRB1 and LILRB2.
SUBCELLULAR LOCATION: Cytoplasmic.
ALTERNATIVE PRODUCTS:
Bent-Alternative splicing; Named isoforms=3;
Name=1; Synonyms=Long;
IsoId=P29350-1; Sequence=Displayed;
                                                              MEDLINE=98380500; PubMed=9712903; Veillette A., Thibaudeau E., Latour S.; Meillette A., Thibaudeau E., Latour S.; High expression of inhibitory receptor SHPS-1 and its association with protein tyrosine phosphatase SHP-1 in macrophages."; J. Biol. Chem. 273:22719-22728(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PTM: Phosphorylated on serine and tyrosine residues.
-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
-!- SIMILARITY: Contains 2 SH2 domains.
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IsoId=P29350-2; Sequence=VSP_005129, VSP_005130;
TISSUE SPECIFICITY: Expressed predominantly in hematopoietic
receptor-mediated signaling in monocytes."; Eur. J. Immunol. 28:3423-3434(1998).
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R INTERPRO: R IPRO03843; TYR_P.

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62;
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01-DEC-1992 (Rel. 24, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein tyrosine phosphatase, non-receptor type 4 (EC 3.1.3.48)
(Protein-tyrosine phosphatase MEG1) (PTPase-MEG1) (MEG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 595;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----LONA-----SPHYONIKEN 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.1%; Score 463; DB 1; L 32.9%; Pred. No. 9.6e-25; ive 56; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            926 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00194; PTPc; 1.
SMART; SM00404; PTPc_motif; 1.
SMART; SM00252; SH2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 32.9%
Matches 112; Conservative
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PDB; 1GWZ; 22-AUG-99.
PDB; 1FPR; 07-MAR-01.
Genew; HGNC:9658; PTPN6.
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Thu Aug 19 09:28:47 2004
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PROTEIN-TYROSINE PHOSPHATASE PHOSPHOCYSTEINE INTERMEDIATE

312 589 926 852

29 517 677 852

Cytoskeleton; Hydrolase

protein;

113-10-02/"YY34-30-118D

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EMBL; M68941; AAA36530.1; -

DR EMBL; BC010674; AAH10674.1; -

DR PIR; A41105; A41105.

HSSP; P29350; 140.2

BR HSSP; P29350; 140.2

BR MIM; 176878; -

DR Genew; HGNC:9656; PTPN4.

BR MIM; 176878; -

DR GO; GO:0006737; C:Cytoplasm; TAS.

GO; GO:0006737; C:Cytoplasm; TAS.

GO; GO:0006737; C:Cytoplasm; TAS.

BR GO; GO:0006737; C:Cytoplasm; TAS.

GO; GO:0006737; C:Cytoplasm; TAS.

GO; GO:0006737; C:Cytoplasm; TAS.

BR HSRO00573; PRO0029; Band 4.1.

BR InterPro; IPR000387; TYR phosphatase.

BR Fam; PF00373; Band 41; 1.

BR PEAM; PR00373; BAND41.

BR PEAM; PR00355; BAND41.

BR PRINTS; PR00595; BAND41.

BR RNAT; SM00295; BAI; 1.

BR RNAT; SM00295; BAI; 1.

BR RNAT; SM00295; BAI; 1.

BR RNAT; SM002065; PERM 1; 1.

BR RNSITE; PS00660; FERM 2; 1.

BR PROSITE; PS00660; FERM 3; 1.

BR PROSITE; PS00065; TYR PHOSPHATASE 1; 1.

BR PROSITE; PS00085; TYR PHOSPHATASE 2; 1.

BR PROSITE; PS00085; TYR PHOSPHATASE 2; 1.

BR PROSITE; PS00085; TYR PHOSPHATASE 2; 1.

BR PROSITE; PS00085; TYR PHOSPHATASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                   A Strouble From M.A.

YESUDESCOLON, M.A.

A REDLINE=2238957; PubMed=12477932;

A Klauener R.D. Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abzamson R.D., Mulahy S.J.,

Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratue P.H.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratue P.H.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grim
"Identification, cloning, and expression of a cytosolic megakaryocyte protein-tyrosine-phosphatase with sequence homology to cytoskeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: May act at junctions between the membrane and the
                                                           orotein 4.1.";
Proc. Natl. Acad. Sci. U.S.A. 88:5867-5871(1991).
                                                                                                                                  SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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-i- FUNCTION: This PTPase activity may directly link growth factor

-i- FUNCTION: This PTPase activity may directly link growth factor

-i- Geoptors and other signaling proteins through protein-tyrosine
phosphorylation. The SHZ regions may interact with other cellular
components to modulate its own phosphatase activity against
interacting substrates (By similarity). May play a positive role
during the stages of erythroid cell proliferation.

-i- CATALITIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Protein-tyrosine phosphatase, non-receptor type 11 (EC 3.1.3.48) (cSH-
                                                                                                                                                                                                                                                                           77 LLQEEGHSDYINGNFIRGVDGSLA----YIATQGPLPHTLLDFWRLVWEFGVKVILMACR
                                                                                                                                                                                                                                                                                                  699 ----KGNEDYINANYINMEIPSSSIINQYIACQGPLPHTCTDFWQMTWEQGSSMVVMLTT
                                                                                                                                                                                                                                                                                                                                                                     191 QYMSWPDRGVPSSPDHMLAMVEBARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    814 OYIAWPDHGVPDDSSDFLDFVCHVRNKRAGKEEPVVVHCSAGIGRTGVLITME--TAMCL
                                                                                                                                                                                                                          133 EIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWINEDIMLRTLKVTFQK--ESRSVYQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                       17 ARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILS
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tyrosine + phosphate.
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
--- TISSUB SPECIFICITY: Expressed in embryonic fibroblast,
hematopoietic, erythroid, myeloid and lymphoid cells.
--- PTW: Phosphorylated by tyrosine-protein kinases (By similarity).
--- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
--- SIMILARITY: Contains 2 SH2 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUB-ERYCHroblast;
MEDLINE=97080566; PubMed=8921851;
MEDLINE=97080566; PubMed=8921851;
MEDLINE=97080566; PubMed=8921851;
MEDLINE=97080566; PubMed=8921851;
"Cloning and expression of the chicken protein tyrosine phosphatase
                                                                                                                                                                     22;
                                                                                                                                 ; Score 462; DB 1; Length 926; Pred. No. 1.9e-24; 47; Mismatches 107; Indels
                                                                                (BY SIMILARITY).; 4DAC6A87A675CFB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 TQMIPPDFSLFDVVLKMRKQRPAAVQTEBQYRFLYHTVAQMF 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   593 AA
                                                                                                   926 AA; 105911 MW;
                                                                                                                                     37.6%;
                                                                                                                                                                       Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTPN11 OR SH-PTP2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHICK
             DOMAIN
DOMAIN
DOMAIN
ACT_SITE
                                                                                                     SEQUENCE
                                                                                                                                       Query Match
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                                                                                                                                                          Local
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
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[9]
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                         NCBI_TaxID=9606;
                                                                                                                                                                                                                        TISSUE=T-cell
    between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                       264
                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 RKEGORQENKNKNRYKNILPFDHTRVVL----HDGDPNEPVSDYINANIMPEFETKCNN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLFCITLIKEKWINEDIMLRTLKVTFQKE---SRSVYQLQYMSWPDRGVPSSPDHMLAMV 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEARRIQGSGPE--PLCVHCSAGCGRTGVLCTVDYVRQLLLIQMIPPDFSLFDVVLKMRK 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGH----SDYINGNFI-----RG
                                                                                                                                                                                                                                                                                                                                                                                                                    212 IKOPLNTTRINAABIESR-VRELSKLABTTDKVKOGFWEEFETLOQOECKLLY-----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 VDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWAQEQEPLQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                440 EEVHHKÕESISDAGPVVVHCSAGIGRIGTFIVIDILIDIIREKGVDCDIDVPKTIQMVRS
                                                                                                                                                                                                                                                                                                                                                                             54; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Protein-tyrosine phosphatase, non-receptor type 11 (EC 3.1.3.48)
(Protein-tyrosine phosphatase 2C) (PTP-2C) (PTP-1D) (SH-PTP3) (SH-
                                                                                                                                                                                                                                                                                                              (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                270 QRPAAVQTEEQYRFLYHTVAQMFCSTLQ------NASPHYQNIK 307
                                                                                                                                                                                                                                                                                                                                                     18.7%; Score 453; DB 1; Length 593; 33.9%; Pred. No. 4.7e-24;
                                                                                                                                                                                                                                                                                                PROTEIN-TYROSINE PHOSPHATASE. PHOSPHOCYSTEINE INTERMEDIATE
                                                                                                                                                                                                                                                                                                                                                                           53; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                415231144BB43DDA CRC64;
                                                                                                                                                                                    Probon; PD000093; SH2; 2.
SWART; SM00194; PTPC; 1.
SWART; SM00194; PTPC; 1.
PROSITE; PS0001; SH2; 2.
PROSITE; PS000383; TYR PHOSPHATASE 1; 1.
PROSITE; PS00056; TYR PHOSPHATASE 2; 1.
PROSITE; PS00056; TYR PHOSPHATASE 2; 1.
HYdrolase; SH2 domain; Repeat; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                593 A.A.
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                                                                        EMBL, U38620; AAC60049.1; -.
HSSP, Q06124; JC5167.
HSSP, Q06124; 2SHP.
INTERPO; IPR000980; SH2.
INTERPO; IPR000387; TYR_phosphatase.
INTERPO; IPR000387; TYR_phosphatase.
Pfam; PP00107; SH2; 2.
Pfam; PP00107; SH2; 2.
Pfam; PP00107; X_phosphatase; 1.
PRINTS; PR00401; SH2DOMAIN.
PCDOm; PD000093; SH2; 2.
                                                                                                                                                                                                                                                                                                                      SIMILARITY
                                                                                                                                                                                                                                                                          SH2 1.
                                                                                                                                                                                                                                                                                                                                 593 AA; 67982 MW;
                                                                                                                                                                                                                                                                                                                                                                 33.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTP2) (SHP-2).
PTPN11 OR PTP2C OR SHPTP2.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 33.9
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                247
459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTNB HUMAN
                                                                                                                                                                                                                                                                                                DOMAIN
ACT_SITE
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MEDLINE=93087502; PubMed=1280823; Freeman R.M. Jr., Plutzky J., Neel B.G.; Identification of a human src homology 2-containing protein-tyrosine-phosphatase: a putative homolog of Drosophila corkscrew."; Proc. Natl. Acad. Sci. U.S.A. 89:11239-11243 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANTS NS GLY-61; CYS-63; GLY-72; SER-72; ASP-76; ARG-79; VAL-282; ASP-308 AND VAL-504.

MEDLINES-1283/43; PubMed=11704759;
Tartaglia M., Mehler E.L., Goldberg R., Zampino G., Brunner H.G., Kremer H., van der Burgt I., Crosby A.H., Ion A., Jeffery S., Kalidas K., Parton M.A., Kucherlapati R.S., Gelb B.D.;
"Mutations in PTPN1, encoding the protein tyrosine phosphatase SHP-2, cause Noonan syndrome."
                                                                                                                                SEQUENCE FROM N.A.
TISSUE-Umbilical cord,
MEDLINE=93211929; PubMed=7681589;
Ashmad S., Barville D.L., Zhao Z., Fischer B.H., Shen S.H.;
"A widely expressed human protein-tyrosine phosphatase containing src
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ullrich A.; "A family of proteins that inhibit signalling through tyrosine kinase
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Bennett A.M., Tang T.L., Sugimoto S., Walsh C.T., Neel B.G.;
"Protein-tyrosine-phosphatase SHPTP2 couples platelet-derived growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with sequence similarity to the src-homology region 2."; FEBS Lett. 314:335-339(1992).
Craniata; Vertebrata; Buteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE="-cell;
MEDLINE=93106179; PubMed=1281790;
Adachi M., Sekiya M., Miyachi T., Matsuno K., Hinoda Y., Imai K.,
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MEDILTE-9402983; PubMed=8216283;
Bastien L., Ramachandran C., Liu S., Adam M.;
"Cloning, expression and mutational analysis of SH-PTP2, human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S.E.;
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MEDLINE-97215901; PubMed-9062191;
Kharitonenkov A., Chen Z., Sures I., Wang H., Schilling J.,
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SEQUENCE FROM N.A.
MEDILINE-93206095; PubMed-7681217;
Vogel W., Lammers R., Huang J., Ullrich A.;
"Activation of a phosphotyrosine phosphatase by tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 1-526.
MEDLINE-98150850; Pubmed=9431886;
MEDLINE-98150850; Dhe-Paganon S., Eck M.J., Shoelson "Crystal structure of the tyrosine phosphatase SHP-2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein-tyrosine phosphatase.";
Biochem, Biophys. Res. Commun. 196:124-133(1993).
                                                                                                                                                                                                                                                                                                                            homology 2 domains.";
Proc. Natl. Acad. Sci. U.S.A. 90:2197-2201(1993)
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us-10-087-993a-36.rsp

P VARIANTS JUML TYR-61; VAL-61; LYS-69; THR-72; VAL-72; ALA-76; GLY-76; LYS-76; VAL-75; ALA-503 AND AG-503, VARIANTS WELDOVEPLASTIC SYNDROWE VAL-60; VAL-61; LYS-69; LEU-71 AND AAR-76, VARIANTS NS ASP-62 AND VAL-60; VAL-61; LYS-69; LEU-71 AND AAR-76, VARIANTS NS ASP-62 AND LEE-73, AND VARIANT ACUTE MYELOID LEUKEMIA LYS-71.

X MEDINNE-28660528; Pubmed=12717436;
A Tartaglia M., Niemeyer C.M., Fragale A., Song X., Buechner J., Jung A., Haehlen K., Hasle H., Licht J.D., Gelb B.D.;
T "Somatic mutations in PyrN11 in juvenile myelomonocytic leukemia, myelodysplastic syndromes and acute myeloid leukemia.";
MAT. Genet. 34:148-150(2003).

-1. FUNCTION: This PyrBase activity may directly link growth factor receptors and other signaling proteins through protein-tyrosine phosphorylation. The Stz regions may interact with other cellular components to modulate its own phosphatase activity against VARIANTS NS ALA-42; ALA-60; ASN-61; GLY-61; ASP-62; CYS-63; GLY-72;

PLE-73; ASP-76; ARG-79; ALA-106; ASP-139; CYS-279; VAL-282; LEU-285;
SER-285; ASP-308; SER-308; VAL-309; LYS-501 AND VAL-282; LEU-285;
SER-285; ASP-308; SER-308; VAL-309; LYS-501 AND VAL-282; LEU-285;
SER-285; ASP-308; SER-308; VAL-309; LYS-501 AND VAL-282; LEU-285;
SER-285; ASP-308; SER-308; VAL-309; LYS-501 AND VAL-304; AND VARIANT

X MEDLINE=21987645; PubMed=11992261;
A van der Burgt I., Brunner H.G., Berton M.A., Gelb B.D.;
A wan der Burgt I., Brunner H.G., Berton M.A., Gelb B.D.;
A wan der Burgt I., Brunner H.G., Berton M.A., Gelb B.D.;
II. Am. J. Hum. Genet. 70:1555-1563(2002).

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II. Am. J. Hum. Genet. 70:1555-1563(2002).

II. Am. J. Hum. Genet. 70:1555-1563(2002).

II. Am. J. Hum. Genet. 70:1555-1563(2002).

II. Am. J. Hum. Genet. 70:1555-1563(2002).

II. Am. J. Hum. Genet. 70:1555-1563(2002).

II. Am. J. Hum. Genet. 70:1555-1563(2002).

II. Marino B., Pizzuti A., Dallapiccola B.;
III. Grouping of multiple-lentigines/LEOFARD and Noonan syndromes on the GLY-76; SYNDROME AND VARIANTS NS GLY-61, CYS-63, SER-72; ILE-73, SER-285 AND ASP-308.
MEDLINE=22151235; PubMed=12161469;
Kosaki K., Suzuki T., Murcya K., Hasegawa T., Sato S., Matsuo N.,
Kosaki R., Nagai T., Hasegawa Y., Ogata T.,
Fin Magai T., Hasegawa Y., Ogata T.,
FIPPN11 (protein-tyrosine phosphatase, nonreceptor-type 11) mutations
in seven Japanese patients with Noonan syndrome.";
J. Clin. Endocrinol. Metab. 87:3529-3533 (2002). interacting substrates. CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein VARIANTS NS ASP-62; CYS-63 AND THR-502.
MEDIJIRE-22256043; PubMed=1225025;
MEDIJIRE-22256043; PubMed=1225025;
Walbelhwari M., Belmont J., Fernbach S., Ho T., Molinari L., Yakub I.
Yu F., Combes A., Towbin J., Craigen W.J., Gibbs R.;
"PIPMYI muterions in Noonan syndrome type I: detection of recurrent muterions in exons 3 and 13 ";
Hum. Mutat. 20:298-304(2002). PIM: Phosphorylation of tyrosine residues at the C-terminus by platelet-derived growth factor creates a binding site for the H.G., domain of GRB2. The DESTABLE of LEOPARD syndrome DISEASE: Defects in PTPN11 are the cause of LEOPARD syndrome tyrosine + phosphate.
SUBUNIT: Binds PTENS1.
SUBCELLULAR LOCATION: Cytoplasmic.
TISSUB SERCIFICITY: Widely expressed; particularly abundant heart, brain, and skeletal muscle. Tartaglia M., Mehler E.L., Goldberg R., Zampino G., Brunner Kremer H., van der Burgt I., Crosby A.H., Ion A., Jeffery S. Kalidas K., Patton M.A., Kucherlapati R.S., Gelb B.D.; Nat. Genet. 29-491-491(2001). Tartaglia M., Mehler E.L., Goldberg R., Zampino G., Brunner Kremer H., van der Burgt I., Crosby A.H., Ion A., Jeffery S. Kaldas K., Patton M.A., Kucherlapati R.S., Gelb B.D.; Nat. Genet. 30:123-123(2001). PTPN11 gene."; Am. J. Hum. Genet. 71:389-394(2002) [14] ERRATUM 

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[MIM:151100], an autosomal dominant disorder allelic with Noonan syndrome. The acronym LEOPARD stands for lentigines, electrocardiographic conduction abnormalities, ocular hypertelorism, pulmonic stenosis, abnormalities of genitalia, retardation of growth, and deafness.

-!- DISMESE: Defects in PrPN11 are a cause of Noonan syndrome [NS]
[MIM:163950]; also designated Noonan syndrome [NS]
[MIM:163950]; also designated Noonan syndrome [NS] is an autosomal dominant disorder characterized by dysmorphic facial features, short stature, hypertelorism, cardac annomalies, deafness, motor delay, and a bleeding diathesis. It is a genetically heterogeneous and relatively common syndrome, with an estimated incidence of 1 in 1000-2500 live births. Wutations in PTPN11 account for more than 50% of the cases. Rarely, NS is associated with juvenile myelomonocytic leukemia (JMML).
-!- DISMESE: Defects in PTPN11 are a cause of Noonan-like syndrome (MIM:163955); also known as Noonan-like/multiple giant cell lesion syndrome. It is an autosomal dominant disorder characterized by noonan features associates with giant cell lesions of bone and This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its work by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-aib.ch/announce/or send an email to license@lsb-sib.ch). 264 154 499 47 94 -!- DISEASE: Defects in PTPN11 are a cause of juvenile myelomonocytic leukemia (JMML) [MIM:607785], a pediatric myelodysplastic syndrome that constitutes approximately 30% of childhood cases of myelodysplastic syndrome (MDS) and 2% of leukemia.
-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
-!- SIMILARITY: Contains 2 SH2 domains. GLFCITLIKEKWLNEDIMLRTLKVTFOKE---SRSVYQLQYMSWPDRGVPSSPDHMLAMV EEARRIQGS--GPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVLKMRK :: |:: | :: | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 48 TVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGH----SDYINGNFI-----RG 1 MSRSLDSARSFLERLEARGGREGAVLA------GEFSDI--QACSAAWKADGVCS 95 VDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWAQEQEPLQT 54; Gaps ORPAAVOTEEQYRFLYHTVAQMFCSTLQ------NASPHYQNIKENCA Length 593; 18.7%; Score 453; DB 1; Length 593 33.8%; Pred. No. 4.7e-24; ive 53; Mismatches 126; Indels EMBL, L08807, -; NOT ANNOTATED CDS.
EMBL, X70766; CAA50045.1;
EMBL, D13540, BAA02740.2;
EMBL, L07527, AAA17022.1;
EMBL, L03535; AAA3611.1; PIR; JN0805; JN0805. PDB; 2SHP; 16-FEB-99. Genew; HGNC:9644; PTPN11. MIM; 176876; -Query Match Best Local Similarity 33.8° Matches 119; Conservative soft tissue 155 212 440 270 g à g à d à g ð 유 ð 셤

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RESULT 15
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Lee C.-H., Kominos D., Jacques S., Margolis B., Schlessinger J.,
Schoelson S.E., Kuriyan J.,
Crystal structures of peptide complexes of the amino-terminal SH2
domain of the Syp tyrosine phosphatase.";
Structure 2:423-438(1994).
-!- FUNCTION: This PTPase activity may directly link growth factor
receptors and other signaling proteins through protein-tyrosine
phosphorylation. The SH2 regions may interact with other callular
components to modulate its own phosphatase activity against
interacting substrates.
-!- CARALYTIC ACTILITY: Protein tyrosine phosphate + H(2)O = protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine + phosphate.
-! SUBMIT: Binds PTRNS1.
-!- SUBMIT: Binds PTRNS1.
-!- SUBGELULAR LOCATION: Cytoplasmic.
-!- PTM: Phosphorylated by tyrosine-protein kinases.
-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
-!- SIMILARITY: Contains 2 SH2 domains.
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

BEDLINE-3206094, PubMed=8096088,
FENG G.-S., Hui C.-C., Pawson T.;
"SH2-containing phosphotyrosine phosphatase as a target of protein-
                                                                                                                                                                                                                     Eukaryota; Metaria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                       U1-FEB-1994 (Rel. 28, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Protein-tyrosine phosphatase, non-receptor type 11 (EC 3.1.3.48)
Protein-tyrosine phosphatase SYP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kharitonenkov A., Chen Z., Sures I., Wang H., Schilling J.,
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| IAYB; 31-AUG-94.
| IAYC; 31-AUG-94.
| IAYD; 31-AUG-94.
| MGI:99511; Ptpn11.
| GO:000515; P:prongenesis; IPI.
| GO:000469; P:axonogenesis; IMP.
| GO:0048011; P:NGF receptor signaling pathway; IMP.
                                                           585 AA.
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Interpro, IPR000387; TYR phosphatase.
Interpro, IPR000242; Tyr_PP.
                                                         PRT;
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PIR; A46209; A46209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97215901; PubMed=9062191;
                                                                                        01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sed
                                                                                                                                                                                                                                                                                                                                                                                            tyrosine kinases.";
Science 259:1607-1611(1993).
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                                                         STANDARD;
                                                                                                                                                                                                              Mus musculus (Mouse)
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PTPNS1 BINDING.
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                                                                                                                                                                                                                                                                 PROTEIN-TYROSINE PHOSPHATASE.
PHOSPHOCYSTEINE INTERMEDIATE (BY
SIMILARITY).
                                                                                                                                                                                                      Hydrolase; SH2 domain; Repeat; Phosphorylation; 3D-structure. DOMAIN 112 216 SH2 DOMAIN 276 S1 PROTEIN-TYROSINE PHOSPHATASE. ACT_SITE 463 463 PHOSPHOCYTEINE INTERMEDIATE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
18.6%; Score 451; DB 1; Length 585;
Best Local Similarity 31.0%; Pred. No. 6.4e-24;
Matches 128; Conservative 59; Mismatches 142; Indels
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                                                                       Probon; PD000093; SH2; 2.
SMART; SM00194; PTPC; 1.
SMART; SM00194; PTPC; 1.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_PTP; 1.
PROSITE; PS50001; SH2; 2.
Pfam; PF00017; SH2; 2.
Pfam; PF00102; Y phosphatase;
PRINTS; PR00700; PRTYPHPHTASE.
PRINTS; PR00401; SH2DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 386:181-186(1997).

-I- FUNCTION: This PTPase activity may directly link growth factor receptors and other signaling proteins through protein-tyrosine phosphorylation. The SH2 regions may interact with other cellular components to modulate its own phosphatase activity against interacting substrates.

-I- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A family of proteins that inhibit signalling through tyrosine kinase receptors.";
                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tyrosine + phosphate.
SUBUNIT: Binds PTPNS:
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
PTM: Phosphorylated by tyrosine-protein kinases (By similarity).
SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
SIMILARITY: Contains 2 SH2 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE.
MEDLINE-93011127; PubMed-1382983;
MISDLINE-93011127; PubMed-1382983;
Miraga A., Munakata H., Hata K., Suzuki Y., Tsuiki S.;
"Purification and characterization of a rat liver protein-tyrosine phosphatase with sequence similarity to src-homology region 2.";
Eur. J. Biochem. 209:195-206(1992).
                                                                           (EC 3.1.3.48)
                                                                                                                                                                                                               STRAIN=Sprague-Dawley,
MEDLINE=54324984; PubMed=8048963;
Ding W., Zhang W.R., Sullivan K., Hashimoto N., Goldstein B.J.,
"Identification of protein-tyrosine phosphatases prevalent in
adipocytes by molecular cloning.",
Biochem. Biophys. Res. Commun. 202:902-907(1994).
                                                                                                                                                                                                                                                                                                                                    STRAIN=Sprague-Dawley,
MEDLINE=94216346; PubMed=7512964;
Mei L., Dorherty C.A., Huganir R.L.;
"RNA splicing regulates the activity of a SH2 domain-containing protein tyrosine phosphatase.";
J. Biol. Chem. 269:12254-12262(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97215901; PubMed=9062191;
Kharitonenkov A., Chen Z., Sures I., Wang H., Schilling J.,
                                                                            7
           P41499; Q62626;
01-NOV-1995 (Rel. 32, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
10-QCT-2003 (Rel. 42, Last annotation update)
Protein-tyrosine phosphatase, non-receptor type:
(Protein-tyrosine phosphatase SyP).
 593 AA
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EMBL; U05963; AAA19133.1; -.
EIR; A53593; A53593.
HSSP; P35235; 1AYA.
InterPro; IPR000980; SH2.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; TYR_PP.
Pfam; PP00017; SH2; 2.
 STANDARD;
                                                                                                                       Rattus norvegicus (Rat)
                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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completed: August 17, 2004, 20:43:12 le : 15 secs

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                                                                                                                                                                                                                                                                     216 SH2 1.

216 SH2 2.

517 PROTEIN-TYROSINE PHOSPHATASE.

459 SIMILARITY).

75 A -> P (IN REF. 1).

407 G -> GQALL (IN REF. 2).

547 Y -> S (IN REF. 2).

547 Y -> S (IN REF. 2).

68033 MW; 3329F10F0F60AF48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
18.5%; Score 448; DB 1; Length 593;
Best Local Similarity 32.7%; Pred. No. 1e-23;
Matches 125; Conservative 57; Mismatches 142; Indels
R Pfam, PF00102; Y_phosphatase; 1.

R PRINTS; PR00700; PRTYPHPHTASE.

R PRINTS; PR00701; PRIZOMAIN.

R PRINTS; PR00701; SH2; 2.

R SMART; SM00194; PTPC; 1.

R SMART; SM00194; PTPC; 2.

R PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.

R PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.

R PROSITE; PS50056; TYR_PHOSPHATASE_PTP; 1.

R PROSITE; PS50010; SH2; 2.

Hydrolase; SH2 domain; Repeat; Phosphorylation.

DOMAIN 6 102 SH2; 2.

HOMAIN 112 216 SH2; 2.

DOMAIN 276 S17 PROFEIN-TYROSINE PHOSPHOYANT ACT_SITE 459 459 PHOSPHOYSTEINE INTER
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593 AA;
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us-10-087-993a-36.rspt

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August 17, 2004, 20:38:19; Search time 43 Seconds (without alignments) 3360.636 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ס			Description	O61152 mus musculu	0922e3 mus musculu	Q7z637 homo sapien		P70602 rattus norv	Q7tmp9 mus musculu	Q9p0u2 homo sapien	Q86xu4 homo sapien	Q80um4 mus musculu	Q63745 rattus norv	Q64642 rattus norv	Q7sy37 brachydanio	Q8biw7 mus musculu	Q15426 homo sapien	Q9hd43 homo sapien	Q9erk5 mus musculu
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	æ.		Length	453	453	351	372	453	802	799	872	775	382	438	592	598	1118	1115	1705
	æ,	Query	Match	73.9	73.5	73.2	73.2	72.4	30.9	30.0	29.2	29.1	29.1	21.1	20.8	20.6	20.3	20.2	20.0
			Score	1791.5	1782.5	1775.5	1775.5	1754.5	749.5	726.5	709	206	705.5	510.5	503.5	498.5	491.5	489.5	485
		Result	No.		7	e	4	Ŋ	9	7	œ	σ	10	11	12	13	14	15	16

Q9uk67 homo sapien	Q9ib94 potamotrygo	Q7zw17 brachydanio	Q9wu22 mus musculu	Q9ib95 potamotrygo	Q64509 mus musculu	Q8n4s3 homo sapien	Q7zyn2 xenopus lae	Q86aj9 dictyosteli	Q803m6 brachydanio	Q92124 xenopus lae	Q91870 xenopus lae	Q9nl15 branchiosto	Q9nl13 branchiosto	Q91871 xenopus lae	Q9jj07 mus musculu	Q8ciw2 mus musculu	Q7zwi6 brachydanio	Q80vn7 mus musculu	O55082 mus musculu	Q9nl05 eptatretus	Q9y406 homo sapien	Q9qwq8 rattus norv	Q9pt91 brachydanio	Q7syn6 brachydanio	Q8mm81 caenorhabdi	Q7tsk0 mus musculu	Q9u3n7 caenorhabdi	Q8av93 petromyzon
Q9UK67	3 Q9IB94	3 Q7ZW17	1 Q9WU22	3 Q9IB95	1 Q64509	Q8N4S3	3 Q7ZYN2					Q9NL15	Q9NL13		1 095507	1 Q8CIW2	3 Q7ZWI6	1 Q80VN7	1 055082	3 Q9NL05	Q9Y406				Q8MM81	1 Q7TSK0	Q9U3N7	3 Q8AV93
624 4	336 13	594 13	926 13	342 13	597 13	292 4	694 13	٠,	589 13		•	470 5	487 5	597 13	•	1998 13	461 13	1102 13	426 1:	473 13	398 4	-	433 13	_	589 5	593 13	624 5	1056 13
19.6	19.5	19.4	19.3	19.1	18.6	18.5	18.4	18.4	18.4	18.3	18.2	18.2	18.2	18.2	18.2	18.1	18.0	17.9	17.8	17.8	17.8	17.7	17.7	17.7	17.7	17.7	17.7	17.7
474.5	471.5	470	469	462	452	449	447	446.5	445.5	444	442	441.5	441	441	440	438	437	433	432.5	431.5	431	430	429	429	428	428	428	428
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### ALIGNMENTS

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TISSUE=KIDNEY,

TISSUE=XIDNEY;

Huang K., Sommers C.L., Grinberg A., Kozak C.A., Love P.E.,

Huang K., Sommers C.L., Grinberg A., Kozak C.A., Love P.E.,

"Cloning and characterization of PTP-KI, a novel nonreceptor protein

"Cloning and characterization of PTP-KI, a novel nonreceptor protein

tyrosine phosphates highly expressed in bone marrow.";

Oncogene 13:1567-1573(1996).

\*\*NT ALTERNATIVE SPLICING.\*\* OG1152, OG2404;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 25, Last annotation update)
01-NOT-2003 (TrEMBLrel. 25, Last annotation update)
Protein-tyrosine phosphatase 18 (EC 3.1.3.48) (PTP-K1) (Fetal liver Protein-tyrosine phosphatase 1) (FIP1) (FTP 49) (PTP HSCF).
Mus musculus (Mouse)
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCRI\_TAXID=10090; RESULT 1 Q61152 

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Best Local Similarity 75.69
Matches 347; Conservative
                                                               PRELIMINARY;
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SEQUENCE 453 AA;
                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                        7; Gaps
         H(2)0 = PROTEIN
                                                                                 ISOId=Q61152-2; Sequence=VSP 050405;
-!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BONE MARROW. ALSO
EXPRESSED IN KIDNEY, LUNG, OVARY, SPLEEN, THYMUS AND LYMPH NODE.
-!- DEVELOPMENTAL STAGE: EXPRESSED IN THE EMBRYO FROM DAY 15.5.
-!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMILY.
                                                                                                                                                           74; Indels
HEMATOPOIETIC CELLS.
CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE +
TYROSINE + PHOSPHATE.
                        SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC. ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2; Name=FLP1A;
                                                                                                                                                                                                                                                                                                                                                                                      73.9%; Score 1791.5; DB 11
75.6%; Pred. No. 5.9e-139;
tive 31; Mismatches 74;
                                                                IsoId=Q61152-1; Sequence=Displayed;
                                                                                                                                        EMBL; U35124; AAB82736.1; -.
EMBL; U49633.1; -.
EMBL; U5223; AAC5291.1; -.
HSSP; Q06124; 2SHP.
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae; McEl_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.5%; Score 1782.5; DB 11; Length 453; 75.6%; Pred. No. 3.2e-138; Live 32; Mismatches 73; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to protein tyrosine phosphatase, non-receptor type 18
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458
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                                                        415 GPDAYEEVTDGAQTGGLGFNLRIGRPKGPRDPPAEWTRV
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
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61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120
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GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLPGRVPADQSPAG 420
                                 181 ÖKESRSVYÖLÖYMSWPDRGVPSSPDHMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.2%; Score 1775.5; DB 4; Length 372; llarity 76.2%; Pred. No. 9.3e-138; Conservative 0; Mismatches 2; Indels 107;
                                                                                                                                                                                                                                                                                                                                      01-UUN-2002 (TrEMBLrel. 21, Created)
01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-UCN-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to protein tyrosine phosphatase, non-receptor type 18
(Brain-derived) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUE=Lymph, and Lymphoma;
Strausberg R.,
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase, Receptor. NON TER 1 SEQUENCE 372 AA, 40708 MW, 417CA80AA054CF8B CRC64;
                                                                                                                               MSRSLDSARSFLERLEARGGREGAVLAGEFS-----
                                                                                                      SGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV
                                                                                                                                                                                                                                                                                       372 AA
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es 349; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                   Last sequence update)
Last annotation update)
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73.2%; Score 1775.5; DB 4
Best Local Similarity 76.2%; Pred. No. 8.6e-138;
Matches 349; Conservative 0; Mismatches 2;
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01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                Homo sapiens (Human)
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                                   RESULT 3
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Strain-C57BL/6NCT: TISSUE-Hematopoletic Stem Cell;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-2288257; PubMed=12477932;

MEDLINE-2288287; M.; Faingold E.A., Grouse L.H., Derge J.G.,

MEDLINE-2288257; PubMed=12477932;

MEDLINE-2588287; Medline F.S., Medline G.M., Manch D., Hong L.,

MEDLINE-2588287; More M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

MEDLINE-2588287; More M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

MEDLINE-2588287; More M.B., More M.G., Malek J.A., Gunarathe P.H.,

MEDLINE-2588287; More M.B., Sodersten R.J., Malek J.A., Glubs R.A.,

Millalon D.K., Muzny D.M., Sodersten B.J., Lu X., Glubs R.A.,

Millalon D.K., Muzny D.M., Sodersten B.J., Lu X., Glubs R.A.,

Millalon D.K., Muzny D.M., Sodersten B.J., Dickson M.C.,

Medling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Millalon D.K., Muzny D.M., Green B.D., Dickson M.C.,

Modriguez A.C., Grimwood J., Grömutz J., Myers R.M., Butterfield Y.S.,

More S.J., Marran M.A.,

Johns S.J., Marran M.A.,

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",
                                GAPAGAGSGTQTGTGTGARSAEBAPLYSKVTPRAQRPGAHAEDARGTLP-GRVPADQSPA 419
                                                                                                                                       361 GA-----SGS-TGPGTRAPNSTDTPIYSQVAPRIQRPVSHTENAQGTTALGRVPADENPS 414
PHYONIKENCAPLYDDALFLRTPQALLAIPRPGGVLRSISVPGSPGHAMADTYAEEQKR
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO55377; AAH55377.1; -.
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                                                                                                                                                                                                                   GSGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Local Similarity 43.7%; Pred. No. 7.3e-53;
les 160; Conservative 55; Mismatches 120;
                                                                                                                                                                                                                                                            415 GPDAYBEVTDGAQTGGLGFNLRIGRPKGPRDPPAEWTRV
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01-0CT-2003 (TrEMBLrel. 25, Last seqn
01-0CT-2003 (TrEMBLrel. 25, Last ann
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                                                             GAPAGAGSGTQTGTGTGTGARSAEEAPLYSKVTPRAQRPGAFAEDARGTLPGRVPADQSPAG 334
                       GAPAGAGSGTQTGTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLPGRVPADQSPAG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 EFGVKVILMACREIENGRKRCERYWAQEQEPLOTGLFCITLIKEKWLNEDIMLRTLKVTF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 TVDYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=97067206; PubMed=8910608;

Aoki N., Yamaquchi-Aoki Y., Ullrich A.;

"The novel protein-tyrosine phosphatase PTP20 is a positive regulator of PC12 cell neuronal differentiation.";

J. Biol. Chem. 271:29422-29426(1996).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSRSIDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOSTIE; PSSOUSS; TYR-PHOSPHAISE_1; 1.

ROSITE; PROCEST EXPICED ACTIVITY; IEA.

GO; GO:0004725; F:Drotein tyrosine phosphatase activity; IEA.

GO; GO:0004725; F:Drotein amino acid dephosphorylation; IEA.

INTERPROFICE PROCOSAS; TYR_Phosphatase.

INTERPROFICE PROCOSAS; TYR_PP.

FIGHT FROM PROCOSAS; TYR_PP.

FRINTS; PROOTOO; PRIYPHPHTASE.

PROSITE; PROOTOO; PRIYPHPHTASE 1; 1.

PROSITE; PROOTOS; TYR_PHOSPHATASE 2; 1.

PROSITE; PROOTOS; TYR_PHOSPHATASE 2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aoki, N, Yamaguchi-Aoki, Y, Ullrich A.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U69673; AAC52896.1; -
HSSP; Q06124; 2SHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           453 AA; 50106 MW; 6CCC132206FB69AE CRC64;
                                                                                                                                                              SGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 372
                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Protein tyrosine phosphatase 20.
Rattus norvegicus (Rat).
                                                                                                                                    SGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV
                                                                                                                                                                                                                                                                                                                             453 AA.
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                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Matches 342; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                         275
                                                                                                                                 421
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31; Gaps

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DVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFG 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYK
                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Protein tyrosine phosphatase, non-receptor type 12 (Fragment).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A STANDARD FROM N.A.

A STRAUBBETG R.,

A STRAUBBETG R.,

STRAUBETG R.,

SUMMILTED ROOM R.,

L. SUMMILTED ROOM R.,

EMBL, BCGSO008; AAHSOOOB.1; -.

EMBL, BCGSO008; AAHSOOOB.1; -.

EMBL, BCGSOOOB; AAHSOOOB.1; -.

EMBL, BCGSOOOB; AAHSOOOB.1; -.

EMBL, BCGSOOOB; AAHSOOOB.1; -.

EMBL, BCGSOOOB; PRICTED ROOM CANDER R.

EN INTERPO; IPROOO35; TYR_PDC MOLIF.

R. INTERPO; IPROOO35; TYR_PDC MOLIF.

R. RAMART; SMOO140; PRICYPHPHTASE.

R. SMART; SMOO140; PRICYPHPHTASE.

R. SMART; SMOO140; PTPC MOLIF; 1.

R. SMART; SMOO140; PTPC MOLIF; 1.

R. SMART; SMOO140; PTPC MOLIF; 1.

R. PROSITE; PSGOOS5; TYR_PHOSPHATASE_1; 1.

R. PROSITE; PSGOOS5; TYR_PHOSPHATASE_2; 1.

R. PROSITE; PSGOOS5; TYR_PHOSPHATASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 YONIKENCAPLYDDALFLRTPQALLAI-----PRPPGGVLRSISVPG 344
266 KWRKORPAAVOTEEOYRFLYHTVAOMF---CSTLONASPHYONIKENCAP 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
29.2%; Score 709; DB 4; Length 87.
Best Local Similarity 40.7%; Pred. No. 1.8e-49;
Matches 143; Conservative 66; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor.
NOW TER 1 1 1 84621458356585D4 CRC64;
SEQUENCE 872 AA, 97952 MW, 84621458356585D4 CRC64;
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                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Q80UM4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 QEQE-PLOTGLECITLIKEKWINEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HMLAMVEEARRLOGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 KMRKORPAAVOTEEOYRFLYHTVAOMFCSTLONASPHYONIKENCAPLYDDALFLRTPOA 325
                                                                                                                                                                                                                  326 LLAIPRPPGGVLRSISVPGS-----PGHAMAD--TYABEQKRGAPAGAGSGTQTGTGTG 377
     HMLAMVERARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84
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                                                                                                                                           27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKWRYKDVLPYDQTRVILSLLQEEGHSDY
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Adrenal gland;
A Huang C., Zhang C., Mu T., Peng Y., Gu Y., Zhang L., Jiang C., Li Huang C., Zhang C., Mu T., Peng Y., Gu Y., Zhang L., Jiang C., Li Huang C., Wang Y., Chen Z., Fu G.;
A novel gene expressed in human adrenal gland.";
Li Submitted (MAY1199) to the EMBL/GenBank/DDBJ databases.
EMBL; AF150732; AAF67472.1; -.
RHSSP; P29350; LGWZ.
RGO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
GO; GO:000470; P:protein mino acid dephosphorylation; IEA.
RO; GO:0006470; P:protein mino acid dephosphorylation; IEA.
RINTERPO; IPR000342; TYR_phosphatase.
R RINTS; PR00700; PRITYPHPHTASE.
R SWART; SM00194; PTPC; 1.
R PROSITE; PS00056; TYR_PHOSPHATASE 1; 1.
R PROSITE; PS00056; TYR_PHOSPHATASE 2; 1.
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30.0%; Score 726.5; DB 4; Length 799;
Best Local Similarity 46.9%; Pred. No. 5.7e-51;
Matches 136; Conservative 56; Mismatches 93; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   799 AA; 90610 MW; 93F5385016F33D0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Protein tyrosine phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   799 AA
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                                                                                                                                                                                                                                                                                                                                                                           363 TMNAEE 368
                                                                                                                                                                                                                                                                                                                             378 ARSAEE 383
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63

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297 364 301

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ESRRLYQFHYVNWPDHDVPSSFDSILDMISLMRKYQEHEDVPICIHCSAGCGRTGAICAI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | : | | | | | 4.25 IDKKLERNLSFEIKKVPLQEGPKSFDGNTLLNRGHAIKIKSASSSVVD----RTSKPQE 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---IPRP-----340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        480 LSAGALKVDDVSQNSCADCSAAHSHRAAESSEESQSNSHTPPRPPDCLPLDKKGHVTWSLH 539
                                                                                                                         365 LIPSPPSAFPTVTTVWQDSDRYHPKPVLHMASPEQHPADLNRSYDKSADPMGKSESAIEH 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----HYONIKENCAPLYDDALFLRT--PQA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   540 GPENATPVPDSPDGKSPDNHSQTLKTVSSTPNSTAEEEAHDLTEHHNSSPLLKAPLSFTN 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARDINESprague-lawley; TISSUE-Kidney;
MEDLINE=95046282; PubMed=7957881;
Moriyama T., Kawanishi S., Inoue T., Imai B., Kaneko T., Xia C.,
Takenaka M., Kamada T., Ueda N.;
"CDNA cloning of a cytosolic protein tyrosine phosphatase (RKPTP) from tat kindney.";
PEBS Lett. 353:305-308(1994).
EMBL; D38072; BAA07266.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          600 PLHSDDSDGGSSDGAVTRNKTSISTASATVSPASSAESACTRRVLPMSIARQEVAGTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :: | :: | | | HSGAEKDADVSEESPPPLPERTPESFVLADMPVRPEWHELPNOEWSEORESEGLTTSGNE
                                                                                                                                                                                                                                                                                                             305 GAQKIADGNEITTGTMVSSIDSEKQDSPPRKPPRTRSCLVEGDAKBEILQPPEPHPVPPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------ADQSPAGSGAYEDVA-GGAQTGGLGFNLRIGRPKGPRDPPAEWT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                       DYVROLLLITQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GAPAGAGSGTQTGTGTGA-----RSAEEAPLYSKVTPR---
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GO, GO:0016787; F:hydrolase activity; IEA.
GO, GO:0004725; F:hydrolase activity; IEA.
GO, GO:0004725; F:protein tyrosine phosphatase activity; IEA.
GO, GO:0006470; P:protein amino acid dephosphorylation; IEA.
InterPro; IPR000387; TYR phosphatase.
InterPro; IPR000242; Tyr_PP.
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                                                                                                                                                                                                                                                                                                                                                                                            ----NASP-----
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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SMART, SMOD194, PTP. 1.
PROSITE: PSO0381 TYR PHOSPHATASE 1;
PROSITE; PSSO056, TYR_PHOSPHATASE_2;
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PRINTS; PR00700; PRTYPHPHTASE.
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Q63745;
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XX MEDINE-2538257; PubMed=12477932;

XI Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

XI strausberg R.L., Collins F.S., Wagner L., Schemmen C.M., Schuler G.D.,

XI Strausberg R.L., Collins F.S., Wagner L., Schemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

And Stapleton M., Soares M.B., Bonaldo M.F., Caravant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Yillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rheby J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rhiching M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rhiching M., Madan A., Young A.C., Schwutz J., Myers R.M., Buterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human and many and mouse on the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESRSVYQLQYMSWPDRGVPSSPDHMLAMVEBARRLQGSGPEPLCVHCSAGCGRTGVLCTV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 VVIIVMACREFEMGRKKCERYWPLYGEDPITFAPFKISCENEQ-ARTDYFIRTLLLEFON 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFG
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strauberg R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.

B Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.

B RG51806, AAH51901.;

GO; GO:0004972; F;Procein tyrosine phosphatase activity; IEA.

GO; GO:0004972; F;Procein amino acid dephosphorylation; IEA.

R GO; GO:0006470; P:procein amino acid dephosphorylation; IEA.

InterPro; IPR003595; PPPC molif.

InterPro; IPR003037; TYR_Phosphatase.

R RHINTS; PR00703; TYR_PPP.

R RART; SM00194; PTPC: 1.

R SMART; SM00194; PTPC: 1.

R PROSITE; PS00193; TYR_PHOSPHATASE 1; 1.

R PROSITE; PS50055; TYR_PHOSPHATASE 2; 1.
        ol-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to protein tyrosine phosphatase, non-receptor type 12.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.1%; Score 706; DB 11; Length 775; 25.1%; Pred. No. 2.7e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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83; Mismatches 162;
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hes 195; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                        ESRSVYQLQYMSWPDRGVPSSPDHMLAMVEEARLQGSGPEPLCVHCSAGCGRTGVLCTV 242
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                                                                                                                                                                                      . .; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SECUENCE FROM N.A. STRAINSMITCH INSURE BRAIN; STRAINSMISTRR, TISSUE=BRAIN; STRAINSMISTRR, THORGAWA H.; Itch S., Okada M., Nakagawa H.; "Iscolation and characterization of a novel membrane-associated protein tyrosine phosphatase-like protein expressed preferentially in the
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation typosine phosphatase)
02 (EC 3.1.3.48) (BEM-2) (Protein-tyrosine-phosphatase) (Phosphotyrosine phosphatase) (Prosphotyrosine phosphatase) (Protein-tyrosine Rattus norvegicus (Rat).
02 (EC 3.1.3.48) (Rat).
03 (EC 3.1.3.48) (Rat).
03 (EC 3.1.3.48) (Rat).
04 (EC 3.1.3.48) (Ratlus)
05 (EC 3.1.3.48) (Ratlus)
06 (EC 3.1.3.48) (Ratlus)
07 (EC 3.1.3.48) (Ratlus)
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09 (EC 3.1.3.48) (Ratlus
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                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQ 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                 DB 11; Length 382;
                                                                            Query Match
29.1%; Score 705.5; DB 11; Length
Best Local Similarity 45.1%; Pred. No. 1.1e-49;
Matches 133; Conservative 59; Mismatches 94; Indels
                                         25A517FDEBB7C344 CRC64;
TYR_PHOSPHATASE_PTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                       382 AA; 44438 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
  PROSITE; PS50055;
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                        Hydrolase.
SEQUENCE
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Q64642;
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REGUENCE FROM N.A.

REGUENCE FROM N.A.

REGUENCE FROM N.A.

STRAIN-AB; TISSUE-Body;

RA Strausberg R.L.; Feingold B.A.; Grouse L.H.; Derge J.G.;

RA Klausner R.D.

A Lischul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

RA Altschul S.F.; Jeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

RA Altschul S.F.; Jordan H.; Moore T., Max S.I.; Wang J.; Hsheh F.;

RA Diatchenko L., Marusina K., Farmer A.A.; Rubin G.M.; Hong L.,

RA Stapleton M.J.; Usdin T.B.; Toshiyuki S., Carninoi P., Prange C.,

RA Raha S.S., Loquellano N.A.; Peters G.J.; Ahramson R.D.; Mullahy S.J.;

RA Raha S.S., Morley K.C.; Hale S., Garcia. A.M.; Gay L.J.; Hulyk S.W.;

RA Rohards S., Worley K.C.; Hale S., Garcia. A.M.; Gay L.J.; Hulyk S.W.;

RA Pahey J.; Helton E.; Ketteman M.; Madan A.; Robeigues S.; Sanchez A.;

Mitting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;

RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Mers R.M.; Butterfield Y.S.;

RA Krzywinski M.I.; Skalska U.; Smallus D.E.; Schnerch A.; Schein J.E.;

RA Krzywinski M.I.; Skalska U.; Smallus D.E.; Schnerch A.; Schein J.E.;
                                                                                                                                                                                        11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 D-YVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQN--- 298
                                                                                                                                                                                                                    69
                                                                                                                                                                                                                                      70 QTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILM
                                                                                                                                                                                                                                                                                                                                                                 23 GAVLAGEFSD-----IQACSAAWKADGVC----STVAGSRPENVRKNRYKDVLPYD
                                                                                                                                                                                                                                                                                                 130 ACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESR--SV
                                                                                                                                                                                                                                                                                                                                                                                                         188 YOLOYMSWPDRGVPSSPDHMLAMVEEARR-----LOGSGPEPLCVHCSAGCGRTGVLCTV
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Actinopteryota; Medazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
NCBI_TaxID=7955;
                                                                                                                                                                                      37; Gaps
                                                                                                         .) (POTENTIAL).
                                                                                                                                                        DB 11; Length 438
                                                            CYTOPLASMIC (POTENTIAL).
PROPELN-TYROSINE PHOSPHATASE.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTEN
SEB7025A4749D6A7 CRC64;
                                                                                                                                                        Score 510.5; DB 11; Length
Pred. No. 1.5e-33;
51; Mismatches 112; Indels
                  EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             592 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 ASPHYQNIKENCAPL-YDDALFLRTPQA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | : | | | | :: | :: | :: ALPAKEATYENVASLVYENASAIRAHES 431
21.1%;
39.0%;
                                                                                                                                                       Query Match
Best Local Similarity 39.0
Matches 128; Conservative
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      NON TER
DOMAIN
DOMAIN
TRANSMEM
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ACT SITE
CARBOHYD
SEQUENCE
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PRINTS; PR00700; PRTYPHPHTASE.
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Q15426;
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUB=COlon;
MEDLINE=2236463. PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
Generation and initial analysis of more than 15,000 full-length human
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Brain-enriched membrane-associated protein tyrosine phosphatase
                                                                                                                                                                                                                                                                           Query Match 20.8%; Score 503.5; DB 13; Length 592; Best Local Similarity 37.1%; Pred. No. 8.6e-33; Matches 117; Conservative 49; Mismatches 110; Indels 39;
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EMBL, AK078884, BAC37443.1; -...
GO:0004712; F:protein tyrosine phosphatase activity; IEA.
GO: GO:000470; P:protein amino acid dephosphorylation; IEA.
InterPro; IPR003961; FN III.like.
InterPro; IPR003951; FN III.like.
InterPro; IPR003951; PTE_motif.
InterPro; IPR00397; TYR_phosphatase.
InterPro; IPR00041; Tyr_PP.
Pfam; PF00041; En3; 2.
Pfam; PF00102; Y_phosphatase; 1.
                                                                                        SEQUENCE FROM N.A.
STRAILSHEAB; TISSUB-Body;
Strailsheab; TISSUB-Body;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BC055139; AAH55139:1; -.
Hypothetical protein:
SEQUENCE 592 AA; 68482 MW; 85A765083105DC7A CRC64;
                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                        cDNA sequences.
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REPUINE—S94124561; PubMed=8294459; MEDLINE—94124561; PubMed=8294459; MEDLINE—94124561; PubMed=8294459; MEDLINE—94124561; PubMed=8294459; MEDLINE—94124561; PubMed=8294459; MEDLINE—94124561; Noguchi H., Mizuno H., Sakamoto C., Kasuga M.; Molecular Cloning of a human transmembrane-type protein tyrosine propharase and its expression in gastrointestinal cancers."; J. Biol. Chem. 269:2075-2081(1994).

B. Biol. Chem. 269:2075-2081(1994).

B. Biol. A49724; A49724; A49724;

Chemey, HGNC:9672; PPERH.

GO: GO:0005807; C:integral to plasma membrane; TAS.

GO: GO:0005001; Fitransmembrane receptor protein tyrosine pho. . .; TAS.

GO: GO:0005001; Fitransmembrane receptor protein tyrosine pho. . .; TAS.

GO: GO:0005001; Fitransmembrane receptor protein tyrosine pho. . .; TAS.

GO: GO:0005001; Fitransmembrane receptor protein tyrosine pho. . .; TAS.

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GO: GO:0005001; Fitransmembrane receptor protein tyrosine pho. . .; TAS.

GO: GO:0006470; Fitransmembrane receptor protein tyrosine pho. . .; TAS.

GO: GO:0006470; Fitransmembrane receptor protein tyrosine pho. . .; TAS.

GO: GO:0006470; Fitransmembrane receptor protein tyrosine pho. . .; TAS.

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GO: GO:0006470; Fitransmembrane receptor protein tyrosine pho. . .; TAS.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                      20.6%; Score 498.5; DB 11; Length 598; 39.7%; Pred. No. 2.3e-32; Ative 50; Mismatches 110; Indels 31;
SMART; SM00060; FN3; 2.
SMART; SM00194; PTPC: mcii; 1.
PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE 2; 1.
PROSITE; PS50056; TYR_PHOSPHATASE PTP; 1.
SEQUENCE 598 AA; 66338 NW; 30Cl320F967D36E6 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Protein tyrosine phosphatase precursor.
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567 PEEAMYENVASLVYENA 583
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Best Local Similarity
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Query Match
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MEDLINE=21328879; PubMed=11435690;

MEDLINE=21328879; PubMed=11435690;

MARINESOR A.G., Mehenni H., Reichenberger E., Antonarakis S.E.,

Krieg T., Olsen B.R.;

"Gene for the human transmembrane-type protein tyrosine phosphatase H

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                    25;
                                                                                                                                                                                                                                                           Query Match 20.3%; Score 491.5; DB 4; Length 1118; Best Local Similarity 43.3%; Pred. No. 2e-31; Matches 116; Conservative 36; Mismatches 91; Indels 25;
                                                                                                                                 1 25 POTENTIAL.
26 1118 PROTEIN TYROSINE PHOSPHATASE.
1118 AA; 123038 MW; F73E3967ECES9F00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 25, Last annotation update)
Transmembrane-type protein tyrosine phosphatase H.
PTPRH.
PS00383; TYR PHOSPHATASE 1; FALSE_NEG. PS50056; TYR_PHOSPHATASE_2; 1. PS50055; TYR_PHOSPHATASE_PTP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 PLPHTLLDFWRLVWFFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITL----I
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R EMBL; AF275148; AAF91411.1; JOINED.
R HSSP; P18052; 17F0.
R GO; GO:0016778; F:Protein tyrosine phosphatase activity; IEA.
GO; GO:0016775; F:Protein tyrosine phosphatase activity; IEA.
GO; GO:0006470; F:Protein tyrosine phosphatase activity; IEA.
GO; GO:0006470; P:Protein maino acid dephosphorylation; IEA.
R InterPro; IPR003961; FW III.
R InterPro; IPR003987; FW III-114e.
R InterPro; IPR003387; TYR_phosphatase.
R InterPro; IPR003387; TYR_phosphatase.
R Pfam; PF001021; Yr_PP.
R Pfam; PF001021; Yr_PP.
R PRIMTS; R000100; PRTPHPHTASE.
R SWART; SW00100; PRTPHPHTASE.
R PROSITE; PS00333; TYR_PHOSPHATASE_1; 1.
R PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
R PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
R PROSITE; PS50056; TYR_PHOSPHATASE_2TP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.2%; Score 489.5; DB 4 40.8%; Pred. No. 2.9e-31; tive 43; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 40.8% Matches 116; Conservative
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Search completed: August 17, 2004, 20:44:08 Job time : 46 secs

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us-10-087-993a-36.rag

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model	August 17, 2004, 20:28:43 ; Search time 54 Seconds (without alignments) 2396.421 Million cell updates/sec
OM protein - p	Run on:

		1 MSRSLDSARSFLERLEARGG
US-10-087-993A-36	2424	1 MSRSLDSARSFLERLEAD
Title:	Perfect score: 2424	Sequence:

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Total number of hits satisfying chosen parameters: 1586107 seqs, 282547505 residues Searched:

1586107

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:\*

1. geneseqp1980s:\*
2. geneseqp2000s:\*
4. geneseqp2001s:\*
5. geneseqp2001s:\*
6. geneseqp2003s:\*
7. geneseqp2003bs:\*
8. geneseqp2003bs:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

цo	Human bra		Human KPP	Rat prote	Partial h	Murine Cy	Human PTP	Human tyr	Mouse isc	Human pro	FLJ20037.	Human Cyt	Human PTP	Human Cyt	Mouse pro	Human PTP	Human mut	Human PTP	Mutant mo	Human PTP	Human pro	Human SID	Human SAP	Human tyr	Human tyr
Description	80	Aaw37254	Adc99051	Aaw49906	Aaw37255	Aay28654	~	Aag78623		Aay67252	Adc64343	Aay28653	Aam51205	Aay28652	Aay67250	Aam51201	Aay67253	Aam51202	Aay67251	Aag78281	Aab59383	Adc64297	Aag78277	Abr43689	Abr43688
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26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	4	45

# ALIGNMENTS

Human brain derived phosphatase 1 (BDP-1). AAW49908 standard; protein; 458 AA 20-JUL-1998 (first entry) AAW49908; RESULT 1
AAW49908
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Brain derived phosphatase 1; BDP-1; human; receptor; protein tyrosine phosphatase; signal transduction; therapy; diagnosis. Homo sapiens

WO9748723-A2.

24-DEC-1997.

96US-0019629P. 96US-0023485P. 96US-0030860P. 96US-0030964P. 96US-0034286P. 97WO-IB000946 17-JUN-1996; 09-AUG-1996; 13-NOV-1996; 15-NOV-1996; 19-DEC-1996; 17-JUN-1997;

(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN

ö Nayler Chen Z, Ullrich A, Kharitonenkov AI, Aoki N, Wang HY, Kim YW;

WPI; 1998-120302/11. N-PSDB; AAV17099.

New phosphatase and kinase enzyme(s) - useful in the diagnosis and treatment of signal transduction disorders.

Claim 11; Fig 3a-d; 138pp; English

This polypeptide comprises a novel human protein tyrosine phosphatase (PTP), designated brain derived phosphatase 1 (BDP-1), that is expressed in most tissues and cell lines at basal level, but expressed high in epithelium origin cell lines and cancer cell lines. The amino acid sequence was deduced from a cDNA clone (see AAV17099) isolated from a haematopoietic MEGO1 cDNA library. The invention relates to novel proteins (see AAW4996-14) involved in cellular signal transduction and to the nucleic acids (see AAV17097-99) coding for them, and provides

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The present sequence represents a novel murine non-receptor protein tyrosine phosphatase of hematopoietic stem cells (PTP HSC). This protein tyrosine phosphatase of hematopoietic stem cells (HSCS) or progenitor cells, and lacks expression in adult tissues. The protein has a N-terminal tyrosine phosphatase domain, followed by a region rich in serine, threonine and proline and a C-terminal region of about 15-25 amino acids which is rich in basic amino acid residues. The protein is capable of tyrosine dephosphorylation in hematopoietic progenitor cells, and functional derivatives of such native tyrosine phosphatases. The progenitor cell can be used in an assay for the identification of PTP HSC or angonists or agonists. The antagonist can be used to induce the interpretation of stem cells, such as undifferentiated malignant can be used for the expansion of undifferentiated stem cells which may facilitate their creatment. The PTP HSC or an agonist antibody against the PTP HSC can be used for the expansion of HSC prior to autologous or heterologus bone constructed stem cells in cell culture themselves the present action of the present action of the present action of the present action of the present action of the present action of the present action of the present action of the present action of the present action of the present action of the present action of the present action of the present action of the expansion of undifferentiated stem cells in vivo undifferentiated stem cells in vivo
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                                                                                                                                                                                                                                                                                                       Haematopoietic stem cell non-receptor protein tyrosine phosphatase - useful for expansion of undifferentiated stem cells in cell culture.
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73.0%; Score 1770.5; DB 2; Length
Best Local Similarity 74.7%; Pred. No. 1.4e-159;
Matches 343; Conservative 32; Mismatches 77; Indels
PTP
                                                                                                                                                                                                                                                                                                                                                             Claim 9; Fig 1; 66pp; English.
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                                                                                                                                              22-MAR-1996;
                                      WO9735019-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "phosphorylated by protein kinases A and C; also
appears to negatively regulate PTPase activity"
229
 vectors, host cells, purified recombinant proteins, methods for identifying compounds that activate or inhibit the novel proteins, as well as methods for the diagnosis and treatment of diseases associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 TVDYVRQLLLITQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS
                                                                                                                                                                                                     1 MSRSLDSARSFLERLEARGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKN
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                                                                                                                                                                                                                                                                        RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW
                                                                                                                                                                                                                                                                                                       61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW
                                                                                                                                                                                                                                                                                                                                               EFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF
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                                                                                                                                                                                                                                                                                                                                                                                                                      OKESRSVYQLQYMSWPDRGVPSSPDHMLAMVEBARRLQGSGPEPLCVHCSAGCGRTGVLC
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                                                                                                                                                                 Gaps
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                                                                                                                          Length 458;
                                                                                                                                                                 Indels
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/note= "Pro, Ser and Thr rich region"
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/note= "tyrosine phosphatase domain"
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                                                                                                                          Score 2411; DB 2;
Pred. No. 1.3e-220;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                          99.5%;
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                                                                                                                                                                 Matches 457; Conservative
                                                         with the novel proteins
                                                                                                                                               Similarity
                                                                                            Sequence 458 AA;
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                                                                                                                              Query Match
Best Local (
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Sequence 353 AA;
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09-AUG-1996;
13-NOV-1996;
15-NOV-1996;
19-DEC-1996;
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AB, Griffin JA;
ee BA, Lee SY;
DB, Arvizu CS;
Tang YT;
Yao MG, Yue H;
                                                                                                                                                                                                                                            anti-HIV; antiallergic; antiinflammatory; antianaemic; antiparkinsonian; nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic; immunosuppressive; anticonvulsant; antiarteriosclerotic; antiartropic; antidabetropic; dermatological; antidabetic; nephrotropic; antigout; thyromimetic; neuroprotective; osteopathic; antiarthritic; antiparasitic; antihelminthic; antipsoriatic; uropathic; ophthalmological, antirheumatic; handsotatic; antibacterial; virucide; protozoacide; fungicide; kinase; phosphatase; KPP; cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis; cancer; developmental; mental retardation; neurological; Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's; diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan; helminthic infection; transgenic; gene therapy; human; enzyme.
GAPAGAGSGTQTGTGARSAEEAPLYSKVTPRAQRPGAHAEDARGTLP-GRVPADQSPA 419
             New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple sclerosis, ostecarthritis, cancer or hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel isolated polypeptide which is a human kinase and phosphatase (KPP). The KPP polypeptides, polymotheotides, agonists and antagonists are useful for diagnosing, treating or preventing cell proliferative disorders such as atherosclerosis, cirrhosis, hepatitis and cancer, developmental disorders e.g. mental retardation, neurological disorders including Alzheimer's disease and Parkinson's disease, autoimmune and inflammatory disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan Emerling BM, Forsythe IJ, Gandhi AR, Gorvad AB, Grif Gurnrajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Zebarjadian Y;
                                                   GSGAYEDVAGGAQTGGLGFNLRIGRPKGPRDPPAEWTRV 458
                                                                  GPDAYEEVTDGAQTGGLGFNLRIGRPKGPRDPPAEWTRV
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                                                                                                                                           ADC99051 standard; protein; 353
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02-NOV-2001; 2001US-0343910P.
13-NOV-2001; 2001US-033998P.
16-NOV-2001; 2001US-0334248P.
30-NOV-2001; 2001US-0334288P.
                                                                                                                                                                                                                       Human KPP protein - SEQ ID 4.
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                                                                                                                                                                                              (first entry)
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N-PSDB; ADC99103.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RYKDVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW
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Crohn's disease and diabetes mellitus and finally, viral, bacterial, fungal, parasitic, protozoan or helminthic infections. Furthermore, tipolymucleotides encoding KPP may be useful for creating transgenic animals to model human disease, as well as during gene therapy procedures. The current sequence is that of the human KPP protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 BFGVKVILMACREIENGRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTF
                                                                                                                                                                                                                                                           Query Match 72.8%; Score 1764.5; DB 7; Length 353; Best Local Similarity 75.9%; Pred. No. 3.7e-159; Matches 349; Conservative 0; Mismatches 2; Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein tyrosine phosphatase; PTP20; rat; signal transduction; cell differentiation; cancer; neural injury; therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Rat protein tyrosine phosphatase PRP20
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96US-0023485P.
96US-0030860P.
96US-0030964P.
96US-0034286P.
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This polypeptide comprises a novel rat protein tyrosine phosphatase, designated PTP20, that regulates growth factor stimulation of cellular differentiation. Its amino acid sequence was deduced from a cDNA clone (see AAV17097) isolated from a rat phaeochromocytoma PC12 cDNA library by PCR amplification using primers based on consensus sequences (see AAV17097) of known PTPs. The invention relates to novel proteins (see AAV17097-99) coding for them, and provides vectors, host acids (see AAV17097-99) coding for them, and provides vectors, host acids (see AAV17097-99) coding for them, as well as methods for the diagnosis and treatment of diseases associated with the novel proteins. Corley PTP20, activators may act as anti-cancer therapeutics that stimulate cell differentiation rather than proliferation, while inhibitors may be useful for treating neural injuries by delaying the differentiation of transplanted neuronal stem cells until they are firmly grafted
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                                                                                                                                                         New phosphatase and kinase enzyme(s) - useful in the diagnosis treatment of signal transduction disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.4%; Score 1754.5; DB 2; Length 453; 74.5%; Pred. No. 4.8e-158; arive 37; Mismatches 73; Indels 7;
                                       Chen Z,
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                                       Wang HY,
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(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
                                       Kharitonenkov AI, Aoki N,
                                                                                                                                                                                                                    Claim 11; Fig 1a-b; 138pp; English
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                                                                                                1998-120302/11.
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                                                                                                                   N-PSDB; AAV17097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 453 AA;
                                   Ullrich A,
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The present sequence represents a partial human non-receptor protein tyrosine phosphatase of hematopoietic stem cells (PTP HSC). This protein tyrosine phosphatase of hematopoietic stem cells (HSCS) or progenitor cells, and lacks expression in adult tissues. The protein has a N-terminal tyrosine phosphatase domain, followed by a region rich in serine, threenine and proline and a C-terminal region of about 15-25 amino acids which is rich in basic amino acid residues. The protein is capable of tyrosine dephosphorylation in hematopoietic progenitor cells, and functional derivatives of such native tyrosine phosphatases. The phosphatase domain of the PTP HSC or a PTP HSC-expressing HSC or progenitor cell can be used in an assay for the identification of PTP HSC or appropriate or agonists. The antagonist can be used to induce the differentiation of stem cells, which may facilitate their hematopoietic cells, e.g. leukaemia cells, which may facilitate their creation of stem cells, antibody against the PTH HSC can be used for the expansion of HSC prior to autologous or heterologous bone marrow transplantation), while the agonist antibody along with a hematopoietic growth factor can be used for the expansion of used for the expansion of used for the expansion of used for the expansion of undifferentiated stem cells in cell when the matopoietic growth factor can be used for the expansion of undifferentiated for the expansion of undifferentiated for the expansion of the object of the expansion of the object of the expansion of the object of the expansion of the object of the expansion of the object of the expansion of the object of the expansion of the object of the expansion of the object of the expansion of the object of the object of the expansion of the object of the expansion of the object of the object of the object of the object of the object of the object of the object of the object of the object of the object of the object of the object of the object of the object of the object of the object of the object of the ob
                                                                                                      Non-receptor protein tyrosine phosphatase, hematopoietic stem cell; PTP HSC; progenitor cell; tyrosine phosphatase domain; PTP HSC agonist; tyrosine dephosphorylation; tyrosine phosphatase; PTP HSC antagonist; stem cell differentiation.
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Best Local Similarity 100.0%; Pred. No. 1.3e-70;
Matches 155; Conservative 0; Mismatches 0;
                                                                 Partial human non-receptor tyrosine phosphatase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Fig 8; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                           97WO-US005278.
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                    (first entry)
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                      09-APR-1998
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61 LLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIEN GRKRCERYWAQEQEPLQTGLFCITLIKEKWLNEDI 155 121

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RESULT

AAW37255 standard; protein; 155

RESULT 5
AAW37255
ID AAW3
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AC AAW3

AAW37255

326 LLAIPRPPGGVLRSISVPGS-----PGHAMAD--TYAEEQKRGAPAGAGSGTQTGTGTG 377 309 QCSIPE-----QSLTVEADSCPLDLPKNAMRDVKTINQHSKQGAEAESTGGSSLGLRTS 362 206 HMLAMVEEARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL 266 KMRKORPAAVOTEEQYRFLYHTVAQMFCSTLONASPHYQNIKENCAPLYDDALFLRTPQA 85 INASFIKGVYGPKAYIATQGPLSTTLLDFWRMIWEYRILVIVWACMEFENGKKKCERYWA 87 INGNEIRGYDGSLAYIATOGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA AAW89247 standard; protein; 807 AA 363 TMNAEE 368 378 ARSAEE 383 10-MAR-1999 Human PTP04 AAW89247; 147 AAW89247 RESULT d 셤 8 쉱 8 셤 δ d ઠે 8 The present protein sequence is that of the murine phosphatase, Z70PEP that has a single catalytic domain. The non-catalytic portion of the phosphatase conclains unique sequences, including five PEST sequences rich in Pro, Glu or Asp, Ser and Thr. Z70PEP shares about 70% sequence identity with the human cytoplasmic phosphatase Lypl. Lyp proteins are important for regulation of T cell antigen and cytokine receptor signalling and for early and late stages of T cell differentiation. Z70PEP has immunosupressive activity. Compounds that increase expression of Lyp protein can be used as immunosupressive agents to reduce or prevent T cell activation or proliferation, to control thymocyte differentiation, to treat autoimmune diseases and transplant situations New nucleic acid encoding intracellular tyrosine phosphatase and related proteins, used to modulate signaling through T cells, particularly as 27. .288 /label= PTPase domain /note= \_catalytic protein tyrosine phosphatase domain" Lymphoid Protein Tyrosine Phosphatase; Lyp protein; lymphoid cell; intracellular tyrosine phosphatase; PTPase; lymphocyte; murine; protein tyrosine kinase; PTKS; immunosuppressant; PEST sequence; T cell antigen receptor signalling; autoimmune disease; transplant; cytokine receptor signalling. Length 802; 31.2%; Score 755.5; DB 2; 44.0%; Pred. No. 1.8e-62; iive 55; Mismatches 119; 689. .695 /label= SH3 binding site /note= "Proline rich sequence" 790. .798 /label= SH3 binding site /note= "Proline rich sequence" Murine Cytoplasmic phosphatase, Z70PEP protein. 613. .621 /label= SH3 binding site /note= "Proline rich sequence" Disclosure, Page 63-64; 105pp; English. Location/Qualifiers Ą AAY28654 standard; protein; 802 98CA-02220853. 99WO-CA000038 (first entry) (HSCR-) HSC RES & DEV LP WPI; 1999-444404/37. immunosuppressant. Sequence 802 AA; Binding-site Binding-site WO9936548-A1 18-JAN-1999; 16-JAN-1998; Binding-site 22-JUL-1999. 01-OCT-1999 Roifman CM; Mus sp Domain AAY28654
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265

QEQE-PLOTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD

FOOT CE.07.60

Snw niii

308

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- useful
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PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding specific protein tyrosine phosphatases for identifying specific modulators for treatment and prevention cancer and neurodegenerative disease.
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, Hui TH;
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97US-0047222P.
97US-0049477P.
97US-00499156P.
97US-0063595P.
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App H,
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11-JUN-1997;
18-JUN-1997;
23-OCT-1997;
                                                                                                                      Homo sapiens
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20-MAY-1997;
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Gaps

31;

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Conservative

Best Local Similarity Matches 161; Conserv

Query Match

86 84

27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY

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Gaps

2

Indels

Score 726.5; DB 4; Pred. No. 1.1e-59; 5; Mismatches 93;

56;

30.0%;

Length 799;

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The present invention provides the protein and coding sequences of human tyrosine phosphatase hPTP. The protein is expressed in human normal suprarenal tissue. The present sequence is the protein of the invention
                                                                          Query Match
Best Local Similarity 46.9
Matches 136; Conservative
                                                    Sequence 799 AA;
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substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA, to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the
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46.9%; Pred. No. 8.6e-60;
tive 56; Mismatches 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 12-13 (Disclosure); 29pp; Chinese
                                                                                                    Human; tyrosine phosphatase; hPTP.
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                               84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method for examining ischaemic conditions; comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive
                                                                                                                                 147 QEQE-PLQTGLFCITLIKEKWLNEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD
                                                                                                                                                  27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY
                    87 INGNFIRGUDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA
                                                                                     85 INANFIKGVYGPEAYIATQGPLSTTLLDFWRMIWEYSVLIIVMACMEYEMGKKKCERYWA
                                                                                                                                                                                                HMLAMVEBARRLQGSGPEPLCVHCSAGCGRTGVLCTVDYVRQLLLTQMIPPDFSLFDVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse ischaemic condition related protein sequence SEQ ID NO:1064
                                                                                                                                                                                                                                                                                                 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse, ischaemia, compressive ischaemia, occlusive ischaemia, vasospastic ischaemia, ischaemic condition, ischaemic disease
                                                                                                                                                                                                                                                                                       :| |||:|||:||| :|| ::|
EMRTQRPSLVQTQEQYELVYNAVLELFKRQMDVIRDKHSGTESQAKHCIP
                                                                                                                                                                                                                                                                  KMRKQRPAAVQTEEQYRFLYHTVAQMF---CSTLQNASPHYQNIKENCAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takahashi Y, Nagata T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 2685-2689; 2690pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                                                                ABB57374 standard; protein; 773
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                                                                                                                                                                                                                                                                                                 264
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ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB57020 to ABB57047) or by determining the expression profile of a gene group comprising these genes. The expression indicator expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic condition-improving drugs or primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                           ESRSVYQLQYMSWPDRGVPSSPDHMLAMVEBARRLQGSGPBPLCVHCSAGCGRTGVLCTV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 EHRRSVMVMKLPLELWSVPLIARRDLSAKAAADSKLPCRRGCQGRNTTATRTSPGATHPD 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365 AITSFSLPNVTTVCRTVTGTTQSQCCTWPHQSNTQPTSTEAMINQRTNGAKSESAIEHID 424
                                                                                                                                                                                                                                                                                                                                                       DVLPYDQTRVILSLLQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                             VVMIVMACREFEMGRKKCERYWPLYGEDPITFAPFKISCENEQ-ARTDYFIRTLLLEFON 184
                                                                                                                                                                                                                                                                                                        425 KKLERNLSFEIKKVPLQEGPKSFDGNTLLNRGHAIKIKSASSSVVDRTSKPQELSÅGALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         485 VDDVSQNSCADCSAAHSHRAAESSEESOSNSHIPPRPDCLPLDKKGHVTWSLHGPENAIP
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                                                                                                                                                                                                                                                                                  9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYK
                                                                                                                                                                                                              29.3%; Score 710; DB 5; Length 773;
25.4%; Pred. No. 3.8e-58;
.ive 88; Mismatches 162; Indels 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYVROLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMF-
                                                                                                                                                                                                             Length 773;
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                                                                                                                                                                             Sequence 773 AA;
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604
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545 VPDSPDGKSPDNHSQTLKTVSSTPNSTAEEEAHDLTEHHNSSPLLKAPLSFTNPLHSDDW
                                                                                    605 HSDGGSSDGAVTRNKTSISTASATVSPASSAESACHRRVLPMSIARQEVAGTPHSGAEKD
                                                                                                                                                                                                                                        HTEASADSPPAFSDXXDQITXSPAEVTDIGFGNRCGKPKGPREPPSEWT 773
                                                                                                                                                                                                                  ----ADOSPAGSGAYEDVA-GGAQTGGLGFNLRIGRPKGPRDPPAEWT
                                           ---GAPAGAGSGTQTGTGA-----RSAEEAPLYSKVTPR--
                                                                                                                                  398 GAHAEDARGTLPGRVP------
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VPGSPGHAMADTY-----AEEQKR-----

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Protein tyrosine phosphatase; PTP; PEST; paxillin binding; adhesion; cell migration; division; cytostatic; antiinflammatory; angiogenesis; cancer; enzyme substrate identification; human.
                                                                                         Human protein tyrosine phosphatase (PTP) PEST amino acid sequence.
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71abel = Pro 5
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/note= "Proline rich
                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  519. .528
/label= Pro 3
/note= "Proline r
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/label= Pro 1
/note= "Proline
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98CA-02238654 98US-0111993P 11-DEC-1998; (UYMC-) UNIV

99WO-CA000461

21-MAY-1999;

02-DEC-1999

31-MAY-1998;

WO9961467-A2

Charest A; Angers-Lousteau A, Cote J, WPI; 2000-097104/08. Tremblay ML,

for treating diseases which are related to cell, inflammation and angiogenesis especially Novel therapeutic agents f proliferation, migration, cancer.

Claim 4; Fig 24; 91pp; English

This is the amino acid sequence of human protein tyrosine phosphatase (PTP) PEST is a soluble PTP that is ubiquitouelly expressed throughout embryonic development and in murine adult tissues. The N-terminal portion of the enzyme encodes for the catalytic domain, while the C-terminal portion is composed of 5 proline rich domains, and a binding site for the adaptor protein Shc. The pro 2 domain is required for paxillin binding, and the synthesis of mutant PTP-PEST have shown that proline 362 is important for paxillin binding activity. The invention relates to a compound that is capable of interfering with the binding of PTP-PEST to signalling molecules that are involved in cell migration, adhesion or division. The compound can be derived from minimal migration, adhesion or division. The compound can be derived from minimal compenses found in binding sites of PTP-PEST. The invention also relates to a method for finding a genuine substrate for an enzyme in a cell that norphaseses the wild type form of the enzyme. A mutant version of PTP-PEST (see AAV67251 and AAV67253) is used in this method. The compounds have cytostatic and antiinflammatory activity. The compounds proliferation, migration, inflammation and angiogenesis, especially proliferation, migration, inflammation and angiogenesis, especially cancer. The novel method is used for identifying a genuine substrate for enzyme

Sequence 780 AA;

AAY67252 standard; protein; 780

RESULT 10
AAY67252
ID AAY67

α

7;

Gaps

26;

Length 780 Indels 63 65 125 182 242 244

tyrosine phosphatase

phosphotyrosine

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99WO-CA000038

18-JAN-1999;

The present invention relates to protein-protein interactions and complexes involved in Transforming Growth Factor (TGF) beta disorders and/or diseases. The complex between two interacting proteins is useful for screening molecules that inhibit TGF beta for diagnosing or treating

Example 16; SEQ ID NO 127; 148pp; English.

diseases or disorders

beta

WO9936548-A1 22-JUL-1999

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126 VVIIVMACREFEMGRKKCERYWPLYGEDPITFAPFKIS-CEDEQARTDYFIRTLLLEFGN 184
                                                                                                                                                                                                                                 64 DVLPYDQTRVILSILQEEGHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFG 123
                                                                                                                                                                                                                                                                                                                                                                                                             DYVRQLLLTQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPH 302
                                                                                                                                                                                                                                                                                                                                                                                                                              diseases or disorders involving TGF beta e.g., hepatitis. To illustrate the invention, Selected interacting Domains (SID) of proteins and their coding sequences were isolated (ADC64243-ADC64318). The present sequence was used to illustrate the irrontion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lymphoid Protein Tyrosine Phosphatase; Lyp protein, immunosuppressant; intracellular tyrosine phosphatase; PTPase; fetal liver; transplant; resting lymphoid cell; protein tyrosine kinase; PTKs; lymphocyte; T cell antigen receptor signalling; cytokine receptor signalling; autoimmune disease; intronic sequence; alternative mRNA splicing;
                                                                                                                                                                         9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYK
                                                                                                                                                                                          | |::|::|
RKFIQRVQAMKSPDHNGEDN--FARDFMRLRRLSTKYRTEKIYPTATGEKEENVKKNRYK
                                                                                                                                                                                                                                                  124 VKVILMACREIENGRKRCERYW-AQEQEPLQTGLFCITLIKEKWLNEDIMLRTLKVTFQK
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                                                                                                             29.2%; Score 709; DB 7; Li
40.7%; Pred. No. 4.7e-58;
ive 66; Mismatches 116;
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27. .289
27. label= PTPase_domain
/note= "Single_catalytic protein i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Cytoplasmic phosphatase, Lyp2 protein.
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                                                                                                                             l Similarity 40.79
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                                                                                 Sequence 780 AA;
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                                                                                                                                                                                                                                                                                                                       DYVROLLITQMIPPDFSLFDVVLKMRKQRPAAVQTEEQYRFLYHTVAQMFCSTLQNASPH 302
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RKFIQRVQAMKSPDHNGEDN--FARDFMRLRRLSTKYRTEKIYPTATGEKEENVKKNRYK 65
                                                                   63
                                                                                                                                                                                                                                                                RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYK
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                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                 303 YQNIKENCAPLYDDALFLRTPQALLAI------PRPPGGVLRSISVPG 344
                                        26;
       Length 780,
      Score 709; DB 3; Length 78
Pred. No. 4.7e-58;
6; Mismatches 116; Indels
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Transforming Growth Factor beta; TGF beta; hepatitis;
Selected Interacting Domain; SID.
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29.2%; Scor
40.7%; Pred
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31-MAY-2002; 2002US-0384537P.
30-OCT-2002; 2002US-0422471P.
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                     Best Local Similarity 40.7
Matches 143; Conservative
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N-PSDB; ADC64342.
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WPI; 2001-570570/64.
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WO200161031-A2.
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                                                                                                                                                      nucleic acid encoding intracellular tyrosine phosphatase and related eins, used to modulate signaling through T cells, particularly as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 EPGEMQLEFGPPSVSCEABK-RKSDYIRTLKVKFNSETRTIYQFHYKNWPDHDVPSSID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 PILELIWDVRCYQEDDSVPICIHCSAGCGRTGVICAIVDYTWMLLXDGIIPENFSVFSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.2%; Score 70%; DB 2; Length 692; 46.7%; Pred. No. 5e-58; ive 54; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PTP-PEST Genbank Accession Number XP034191.
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                                                                                                                                                                                                                         Claim 4b; Page 55; 105pp; English.
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 98CA-02220853.
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Matches 136; Conservative
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                                (HSCR-) HSC RES & DEV LP
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                                                                                                  WPI; 1999-444404/37, N-PSDB; AAX90696.
                                                                                                                                                                        proteins, used to immunosuppressant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 692 AA;
 16-JAN-1998;
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                                                                   Roifman CM
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ID AAM5
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The invention relates to identifying agents which alter the interaction between a protein tyrosine phosphatase (PTP) and a tyrosine phosphatase (PTP) and a tyrosine phosphatylated polypeptide using fluorescence energy signals. The methods are useful for performing screening assay to identify agents that alter PTP binding to and PTP-mediated catalytic dephosphorylation of phosphotyrosine peptide substrates. The present sequence is not given in the specification but is that of human PTP-PEST protein sequence taken from Genbank (Accession Number; XP034191). The present sequence was used to generate mutants D199A (AAMS1201) and C231S (AAMS1202) as described in the specification. Note: An alternative sequence for human PTP-PEST is given in figure 1 of the specification (AAG7821)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304
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                                                                                                                                                                                                                                                                                        Screening assays to identify agents that alter protein tyrosine phosphatase (PTP) binding to, and PTP-mediated catalytic dephosphorylation of phosphotyrosine peptide substrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.2%; Score 708; DB 4; Length 78
40.7%; Pred. No. 5.9e-58;
ive 66; Mismatches 116; Indels
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13-FEB-2001; 2001WO-US005180
                                                   14-FEB-2000; 2000US-0181769P.
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Best Local Similarity 40.7%;
Matches 143; Conservative
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transplant situations
                                                                                      Sequence 808 AA;
                                            22-JUL-1999
                                                      Roifman CM
         Key
Domain
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               Domain
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05-APR-2000
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11-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding intracellular tyrosine phosphatase and related proteins, used to modulate signaling through T cells, particularly as immunosuppressant.
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Tabel= PEST sequence
10. 10. Or Asp, Ser and Thr"
11. 745
                                                                                                                                                                                                                                       77. .289
Vidael= PTPase_domain
Ynote= Single catalytic protein tyrosine phosphatase
                                                                                                                                                                                                                                                                                                                                    469.472
/label= MXXX_motif
/label= MXXX_motif
horde= "Unique sequence recognised by phosphotyrosine
binding (PTB) domain"
615...623
/label= SHB binding site
/note= "Proline rich sequence"
694...701
/label= SHB binding site
/label= SHB binding site
/label= "Proline rich sequence"
Lymphoid Protein Tyrosine Phosphatase; Lyp protein; lymphoid cell; intracellular tyrosine phosphatase; PTPase; lymphocyte; thymcoyte; T cell; B cell; protein tyrosine kinase; PTKs; immunosuppressant; T cell antigen receptor signalling; cytokine receptor signalling; autoimmune disease; transplant:
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768.
/label= SH3 binding site
/arte= "Proline rich sequence"
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|label= SH3 binding site
|note= "Proline rich sequence"
                                                                                                                                                                                                            ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                              domain"
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N-PSDB; AAX90695.
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                                                                                                                              205
                                                                                                203
                                                                                                                                                                                    HMLAMVEBARRLOGSGPEPLCVHCSAGCGRTGVLCT-VDYVRQLLLTQMIPPDFSLFDVV 264
                                           98
                                                               84
                                                                                                                                           145 EPGEMQLEFGPFSVSCEAEK-RKSDYIIRTLKVKFNSETRTIYQFHYKWWPDHDVPSSID
                                          AGEFSD1QACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLQEEGHSDY
                                                        25 ANEFLKLKRQSTKYKADKTYPTTVAENAKNIKKNRYKDILPYDYSRVELSLITSDEDSSY
                                                                                     87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVWEFGVKVILMACREIENGRKRCERYWA
                                                                                                                               QEQE-PLOTGLFCITLIKEKWINEDIMLRTLKVTFQKESRSVYQLQYMSWPDRGVPSSPD
                                                                                                                                                                                                                                                                                                                                                                              Protein tyrosine phosphatase; PTP; PEST; paxillin binding; adhesion; cell migration; division; cytostatic; antiinflammatory; angiogenesis; cancer; enzyme substrate identification; mouse.
                      Gaps
                                                                                                                                                                                                                                                                                                                                                            Mouse protein tyrosine phosphatase (PTP) PEST amino acid sequence.
                                                                                                                                                                                                                             264 REMRIQRPSLVQTQEQYELVYNAVLELFKRQMDVIRDKHSGTSSQAKHCIP 314
                                                                                                                                                                                                                   LKWRKQRPAAVQTEEQYRFLYHTVAQMF---CSTLQNASPHYQNIKENCAP 312
                        9
  Length 808;
                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Charest A;
                      95;
; Score 708; DB 2;
; Pred. No. 6.2e-58;
54; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        .32. .339
|Tabel= Pro 1
|note= "Proline rich domain 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /64. .771
/label= Pro 5
/~rte= "Proline rich domain 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J55. .364
/label= Pro_2
/~~re= "Proline rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
519. .528
/label= Pro_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       675. .681
/label= Pro 4
'.~+e= "Proline r
                                                                                                                                                                                                                                                                                             AAY67250 standard; protein; 775
29.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-CA000461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98CA-02238654
98US-0111993P
  Query Match
Best Local Similarity 46.74
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cote J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UYMC-) UNIV MCGILL.
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Novel therapeutic agents for treating diseases which are related to cell proliferation, migration, inflammation and angiogenesis especially cancer

24; 91pp; English Claim 4; Fig

This is the amino acid sequence of mouse protein tyrosine phosphatase (PTP) PEST is a soluble PTP that is ubiquitously expressed throughout embryonic development and in murine adult tissues. The Netroughout embryonic development and in murine adult tissues. The Netroughout embryonic development and in murine adult tissues. The Netroughout embryonic development and in murine adult tissues. The Netroughout embryonic of composed of 5 proline rich domain, while the Composular proline side for the adaptor protein Shor. The pro 2 domain is required for paxillin binding and the synthesis of mutant PTP-PEST have shown that proline 322 is important for paxillin binding activity. The invention relates to a compound that is capable of interfering with the binding of PTP-PEST to signalling molecules that are involved in cell migration, adhesion or division. The compound can be derived from minimal expresses the wild type form of PTP-PEST. The invention also relates to a method for finding a genuine substrate for an enzyme in a cell that normally expresses the wild type form of the enzyme. A mutant version of PTP-PEST (see AAY67251 and AAY67253) is used in this method. The compounds have cytostatic and antiniflammatory activity. The compounds can be used for making medicaments for treating a disease related with cell proliferation, migration, inflammation and angiogenesis, especially cancer. The novel method is used for identifying a genuine substrate for an enzyme 

Sequence 775 AA;

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29.1%; Score 705; DB 3; Length 775; 25.0%; Pred. No. 1.1e-57; ive 84; Mismatches 162; Indels 336; Gaps Cuery Match Best Local Similarity 25.09 Matches 194; Conservative

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GAPAGAGSGTQTGTGTGARSABEAPLYSKVTPR 393	600 PLHSDDWHSDGGSSDGAVTRNKTSISTASATVSPASSAESACHRRVLPMSIARQEVAGTP 659	394AQRPGAHAEDARGTLPGRVP	660 HSGAEKDADVSEESPPPLPERTPESFVLADMPVRPEWHELPNQEWSEQRESEGLTTSGNE 719	ADQSPAGSGAYEDVA-GGAQTGGLGFNLRIGRPKGPRDPPAEWT 456	720 KHDAGGIHTEASADSPPAFSDKKDQITKSPAEVTDIGFGNRCGKPKGPREPPSEWT 775	
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